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SEQUENCE LISTING

<110> Sheppard, Paul O.
Presnell, Scott R.

<120> MAMMALIAN SECRETED PROTEINS

<130> 00-41

<150> US 60/215,446

<151> 2000-06-30

<160> 329

<170> FastSEQ for Windows Version 3.0

 $\langle 210 \rangle$ 1

<211> 453

<212> DNA

<213> Homo sapiens

 $\langle 220 \rangle$

<221> CDS

<222> (1)...(453)

<400> 1

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Met Leu Phe Pro Gly Leu Thr Thr Thr Leu Leu Leu Leu Val Phe Phe
1 5 10 15

ctg ctg gtt ttc tcc ctg cct gct ggc cta cat aca gcc ctc aca gca 96
Leu Leu Val Phe Ser Leu Pro Ala Gly Leu His Thr Ala Leu Thr Ala
20 25 30

gcc aga gga ctc ccc aaa ctg ccc aag cac agc cac atc gcc aaa gac 144
Ala Arg Gly Leu Pro Lys Leu Pro Lys His Ser His Ile Ala Lys Asp
35 40 45

acc cat tca tcc ttc cca tct cag ctc cag ggg ctg ctt tcc aaa gca 192
Thr His Ser Ser Phe Pro Ser Gln Leu Gln Gly Leu Leu Ser Lys Ala
50 55 60

Met	Leu	Phe	Pro	Gly	Leu	Thr	Thr	Thr	Leu	Leu	Leu	Leu	Val	Phe	Phe
1				5					10					15	
Leu	Leu	Val	Phe	Ser	Leu	Pro	Ala	Gly	Leu	His	Thr	Ala	Leu	Thr	Ala
			20					25					30		
Ala	Arg	Gly	Leu	Pro	Lys	Leu	Pro	Lys	His	Ser	His	Ile	Ala	Lys	Asp
		35					40					45			
Thr	His	Ser	Ser	Phe	Pro	Ser	Gln	Leu	Gln	Gly	Leu	Leu	Ser	Lys	Ala
	50					55					60				
Thr	Pro	His	Arg	His	Pro	Cys	Asp	Ile	Ala	Gln	Phe	Lys	Thr	Val	Arg
65					70					75					80
Ile	Gln	Glu	Ser	Gln	Gln	Gln	Val	Val	Thr	Lys	Arg	Lys	Phe	Gln	His
				85					90					95	

Phe Thr Ala Ile His Arg Gln Gly Ser Tyr Val Tyr Gln Asp Asn Arg
 100 105 110
 Arg Thr Thr Glu His Arg Pro Ser Ser Ala Val Leu Leu Leu Pro Phe
 115 120 125
 Ala Leu Phe Pro Gln Lys His Val Ile Phe Val Arg Pro Leu Ser Val
 130 135 140
 Val Leu Leu Phe Ala Leu
 145 150

<210> 3
 <211> 303
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (1)...(303)

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 Met Glu Ile Leu His Asn Glu Ile Ser Glu Leu Glu Ser Leu Thr Leu
 1 5 10 15

gtc cct ccc ctc atc ttc tta ctt tta ccc agc aga tct acc cgt ggg 96
 Val Pro Pro Leu Ile Phe Leu Leu Leu Pro Ser Arg Ser Thr Arg Gly
 20 25 30

cag ccc ttt tcc caa gta cca ggg gag aaa atg gat tca gaa aag gat 144
 Gln Pro Phe Ser Gln Val Pro Gly Glu Lys Met Asp Ser Glu Lys Asp
 35 40 45

ttg tgg gga gag gag ctt cca cac tta ata ctg aaa gag gct ttt cat 192
 Leu Trp Gly Glu Glu Leu Pro His Leu Ile Leu Lys Glu Ala Phe His
 50 55 60

ctg ttt ttc aag cca aca gca gcc cca ttc cca gat tca ctc aag gtc 240
 Leu Phe Phe Lys Pro Thr Ala Ala Pro Phe Pro Asp Ser Leu Lys Val
 65 70 75 80

tcc ctt aca tgt ccc tgg aaa gaa gga ggg tca cat aca aga tgc cag 288
 Ser Leu Thr Cys Pro Trp Lys Glu Gly Gly Ser His Thr Arg Cys Gln
 85 90 95

F00230-222860

303

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<210> 4
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<212> PRT
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<220>
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<222> (1)...(276)

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Met	Ser	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	
1				5					10					15		
ctg	ttt	aaa	tgg	aaa	aga	aga	gta	gta	agt	ggt	cat	ctt	ctc	agc	gtc	96
Leu	Phe	Lys	Trp	Lys	Arg	Arg	Val	Val	Ser	Gly	His	Leu	Leu	Ser	Val	
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<221> CDS

<222> (1)...(591)

<400> 7

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1				5					10					15		
tgg	gcc	tcc	gtg	agc	gcc	cag	acc	gat	gcc	acc	ccg	gcg	gtg	acg	aca	96
Trp	Ala	Ser	Val	Ser	Ala	Gln	Thr	Asp	Ala	Thr	Pro	Ala	Val	Thr	Thr	
			20					25					30			
gag	ggc	ctc	aac	tcc	acc	gag	gca	gcc	ctg	gcc	acc	ttc	gga	act	ttc	144
Glu	Gly	Leu	Asn	Ser	Thr	Glu	Ala	Ala	Leu	Ala	Thr	Phe	Gly	Thr	Phe	
			35				40					45				
ccg	tcg	acc	agg	ccc	ccc	ggg	act	ccc	agg	gct	cca	ggg	ccc	tcc	tcc	192
Pro	Ser	Thr	Arg	Pro	Pro	Gly	Thr	Pro	Arg	Ala	Pro	Gly	Pro	Ser	Ser	
	50					55				60						
ggc	ccc	agg	cct	acc	cca	gtc	acg	gac	gtt	gct	gtt	ctc	tgt	gtc	tgt	240
Gly	Pro	Arg	Pro	Thr	Pro	Val	Thr	Asp	Val	Ala	Val	Leu	Cys	Val	Cys	
65					70				75					80		
gac	tta	tcc	cca	gca	cag	tgt	gac	atc	aac	tgc	tgc	tgt	gat	ccc	gac	288
Asp	Leu	Ser	Pro	Ala	Gln	Cys	Asp	Ile	Asn	Cys	Cys	Cys	Asp	Pro	Asp	
				85					90					95		
tgc	agc	tcc	gtg	gat	ttc	agt	gtc	ttt	tct	gcc	tgc	tca	gtt	cca	gtt	336
Cys	Ser	Ser	Val	Asp	Phe	Ser	Val	Phe	Ser	Ala	Cys	Ser	Val	Pro	Val	
			100					105					110			
gtc	aca	ctt	act	gga	gct	ctc	ccg	tgt	cag	ctc	gta	gca	cag	aag	gtg	384
Val	Thr	Leu	Thr	Gly	Ala	Leu	Pro	Cys	Gln	Leu	Val	Ala	Gln	Lys	Val	
			115				120					125				
aag	agc	ctg	ctg	tgg	ggc	cag	ggc	ttc	cca	gat	tac	gtg	gcc	cct	ttt	432
Lys	Ser	Leu	Leu	Trp	Gly	Gln	Gly	Phe	Pro	Asp	Tyr	Val	Ala	Pro	Phe	
	130					135				140						
gga	aat	tcc	cag	gcc	cag	gac	atg	ctg	gac	tgg	tgc	cca	tcc	act	tca	480
Gly	Asn	Ser	Gln	Ala	Gln	Asp	Met	Leu	Asp	Trp	Cys	Pro	Ser	Thr	Ser	
145					150					155					160	

09093737 06001

528

576

591

[illegible]

<400> 8															
Met 1	Arg	Pro	Arg	Gly 5	Leu	Pro	Pro	Leu	Leu 10	Val	Val	Leu	Leu	Gly 15	Cys
Trp	Ala	Ser	Val 20	Ser	Ala	Gln	Thr	Asp 25	Ala	Thr	Pro	Ala	Val 30	Thr	Thr
Glu	Gly	Leu	Asn 35	Ser	Thr	Glu	Ala 40	Ala	Leu	Ala	Thr	Phe 45	Gly	Thr	Phe
Pro	Ser	Thr	Arg	Pro	Pro	Gly 55	Thr	Pro	Arg	Ala	Pro	Gly 60	Pro	Ser	Ser
Gly 65	Pro	Arg	Pro	Thr	Pro	Val 70	Thr	Asp	Val	Ala	Val 75	Leu	Cys	Val 80	Cys
Asp	Leu	Ser	Pro	Ala 85	Gln	Cys	Asp	Ile	Asn 90	Cys	Cys	Cys	Asp	Pro 95	Asp
Cys	Ser	Ser	Val 100	Asp	Phe	Ser	Val	Phe 105	Ser	Ala	Cys	Ser	Val 110	Pro	Val
Val	Thr	Leu	Thr 115	Gly	Ala	Leu	Pro 120	Cys	Gln	Leu	Val 125	Ala	Gln	Lys	Val
Lys	Ser	Leu	Leu	Trp	Gly	Gln 135	Gly	Phe	Pro	Asp	Tyr 140	Val	Ala	Pro	Phe
Gly 145	Asn	Ser	Gln	Ala	Gln	Asp 150	Met	Leu	Asp	Trp	Cys 155	Pro	Ser	Thr 160	Ser
Ser	Pro	Ser	His 165	Ser	Thr	Gly	Arg	Trp	Cys 170	Asp	Glu	Gly	Ser	Arg 175	Gly
Ser	Gln	Leu	Leu	Arg	Arg	Gln	Asp	Gly	Pro	Glu	Trp	Glu	Arg	Gly	Leu

190

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<220>
<221> CDS
<222> (1)...(1200)
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<400> 9

ccg ctg tgg tcc tcc tca ctg cct ggg ctg gac act gct gaa agt aaa 96
Pro Leu Trp Ser Ser Ser Leu Pro Gly Leu Asp Thr Ala Glu Ser Lys
20 25 30

gcc acc att gca gac ctg atc ctg tct gcg ctg gag aga gcc acc gtc 144
Ala Thr Ile Ala Asp Leu Ile Leu Ser Ala Leu Glu Arg Ala Thr Val
35 40 45

ttc cta gaa cag agg ctg cct gaa atc aac ctg gat ggc atg gtg ggg 192
Phe Leu Glu Gln Arg Leu Pro Glu Ile Asn Leu Asp Gly Met Val Gly
50 55 60

gtc cga gtg ctg gaa gcc ctg cgt gaa tgc tct cac tcg gat gtt ctc 240
Val Arg Val Leu Glu Ala Leu Arg Glu Cys Ser His Ser Asp Val Leu
65 70 75 80

act cat gtc tcc cca att tct ggc cac ctc tgg atc ttc acc att gtc 288
Thr His Val Ser Pro Ile Ser Gly His Leu Trp Ile Phe Thr Ile Val
85 90 95

tcc cac ctc aac aaa gcc act gct agc cca cag gag cag cta aaa agt 336
Ser His Leu Asn Lys Ala Thr Ala Ser Pro Gln Glu Gln Leu Lys Ser
100 105 110

gtc cgg gag aag tgg gcc cag gag ccc ctg ctg cag ccg ctg agc ctg 384

Val	Arg	Glu	Lys	Trp	Ala	Gln	Glu	Pro	Leu	Leu	Gln	Pro	Leu	Ser	Leu		
		115					120					125					
cgc	gtg	ggg	atg	ctg	ggg	gag	aag	ctg	gag	gct	gcc	atc	cag	aga	tcc	432	
Arg	Val	Gly	Met	Leu	Gly	Glu	Lys	Leu	Glu	Ala	Ala	Ile	Gln	Arg	Ser		
	130					135					140						
ctc	cac	tac	ctc	aag	ctg	agt	gat	ccc	aag	tac	cta	aga	gag	ttc	cag	480	
Leu	His	Tyr	Leu	Lys	Leu	Ser	Asp	Pro	Lys	Tyr	Leu	Arg	Glu	Phe	Gln		
145					150					155					160		
ctg	acc	ctc	cag	ccc	ggg	ttt	tgg	aag	ctc	cca	cat	gcc	tgg	atc	cac	528	
Leu	Thr	Leu	Gln	Pro	Gly	Phe	Trp	Lys	Leu	Pro	His	Ala	Trp	Ile	His		
				165					170					175			
act	gat	gcc	tcc	ttg	gtg	tac	ccc	acg	ttc	ggg	ccc	cag	gac	tca	ttc	576	
Thr	Asp	Ala	Ser	Leu	Val	Tyr	Pro	Thr	Phe	Gly	Pro	Gln	Asp	Ser	Phe		
			180					185					190				
tca	gag	gag	aga	agt	gac	gtg	tgc	ctg	gtg	cag	ctg	ctg	gga	acc	ggg	624	
Ser	Glu	Glu	Arg	Ser	Asp	Val	Cys	Leu	Val	Gln	Leu	Leu	Gly	Thr	Gly		
		195					200					205					
acg	gac	agc	agc	gag	ccc	tgc	ggc	ctc	tca	gac	ctc	tgc	agg	agc	ctc	672	
Thr	Asp	Ser	Ser	Glu	Pro	Cys	Gly	Leu	Ser	Asp	Leu	Cys	Arg	Ser	Leu		
	210					215					220						
atg	acc	aag	ccc	ggc	tgc	tca	ggc	tac	tgc	ctg	tcc	cac	caa	ctg	ctc	720	
Met	Thr	Lys	Pro	Gly	Cys	Ser	Gly	Tyr	Cys	Leu	Ser	His	Gln	Leu	Leu		
225					230					235					240		
ttc	ttc	ctc	tgg	gcc	aga	atg	agg	ggg	tgc	aca	cag	gga	cca	ctc	caa	768	
Phe	Phe	Leu	Trp	Ala	Arg	Met	Arg	Gly	Cys	Thr	Gln	Gly	Pro	Leu	Gln		
				245					250					255			
cag	agc	cag	gac	tat	atc	aac	ctc	ttc	tgc	gcc	aac	atg	atg	gac	ttg	816	
Gln	Ser	Gln	Asp	Tyr	Ile	Asn	Leu	Phe	Cys	Ala	Asn	Met	Met	Asp	Leu		
			260					265					270				
aac	cgc	aga	gct	gag	gcc	atc	gga	tac	gcc	tac	cct	acc	cgg	gac	atc	864	
Asn	Arg	Arg	Ala	Glu	Ala	Ile	Gly	Tyr	Ala	Tyr	Pro	Thr	Arg	Asp	Ile		
		275					280					285					

ttc atg gaa aac atc atg ttc tgt gga atg ggc ggc ttc tcc gac ttc 912
 Phe Met Glu Asn Ile Met Phe Cys Gly Met Gly Gly Phe Ser Asp Phe
 290 295 300

tac aag ctc cgg tgg ctg gag gcc att ctc agc tgg cag aaa cag cag 960
 Tyr Lys Leu Arg Trp Leu Glu Ala Ile Leu Ser Trp Gln Lys Gln Gln
 305 310 315 320

gaa gga tgc ttc ggg gag cct gat gct gaa gat gaa gaa tta tct aaa 1008
 Glu Gly Cys Phe Gly Glu Pro Asp Ala Glu Asp Glu Glu Leu Ser Lys
 325 330 335

gct att caa tat cag cag cat ttt tcg agg aga gtg aag agg cga gaa 1056
 Ala Ile Gln Tyr Gln Gln His Phe Ser Arg Arg Val Lys Arg Arg Glu
 340 345 350

aaa caa ttt cca gat ggc tgc tcc tcc cac aac aca gcc aca gca gtg 1104
 Lys Gln Phe Pro Asp Gly Cys Ser Ser His Asn Thr Ala Thr Ala Val
 355 360 365

gca gcc ctg ggt ggc ttc cta tac atc ctg gca gaa tac ccc cca gca 1152
 Ala Ala Leu Gly Gly Phe Leu Tyr Ile Leu Ala Glu Tyr Pro Pro Ala
 370 375 380

aac aga gag cca cac cca tcc aca ccg cca cca cca agc agc cgc tga 1200
 Asn Arg Glu Pro His Pro Ser Thr Pro Pro Pro Pro Ser Ser Arg *
 385 390 395

<210> 10

<211> 399

<212> PRT

<213> Homo sapiens

<400> 10

Met Ala Ser Leu Gly Leu Leu Leu Leu Leu Leu Leu Thr Ala Leu Pro
 1 5 10 15
 Pro Leu Trp Ser Ser Ser Leu Pro Gly Leu Asp Thr Ala Glu Ser Lys
 20 25 30
 Ala Thr Ile Ala Asp Leu Ile Leu Ser Ala Leu Glu Arg Ala Thr Val
 35 40 45
 Phe Leu Glu Gln Arg Leu Pro Glu Ile Asn Leu Asp Gly Met Val Gly
 50 55 60

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<222> (1)...(243)

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Met	Ala	Ala	Pro	Lys	Gly	Leu	Leu	Leu	Val	Ala	Leu	Val	Leu	Leu	Leu	
1			5			10			15							
gct	gac	agc	ttg	cag	gtg	att	agt	ggg	aaa	gct	cag	tgt	gtg	act	gct	96
Ala	Asp	Ser	Leu	Gln	Val	Ile	Ser	Gly	Lys	Ala	Gln	Cys	Val	Thr	Ala	
20			25			30										
gtg	act	ttg	gct	att	ccc	aca	cag	aga	aat	gtg	gca	cca	agg	tgc	ttt	144
Val	Thr	Leu	Ala	Ile	Pro	Thr	Gln	Arg	Asn	Val	Ala	Pro	Arg	Cys	Phe	
35			40			45										
ggg	gag	gat	gca	caa	gtg	gca	gcc	tcc	tgc	aag	atg	ctg	aag	gac	ttt	192
Gly	Glu	Asp	Ala	Gln	Val	Ala	Ala	Ser	Cys	Lys	Met	Leu	Lys	Asp	Phe	
50			55			60										
ttg	ctg	gtt	gca	ctg	gcc	ttc	act	ggt	gtc	act	ctg	ttg	ctg	ctc	ctg	240
Leu	Leu	Val	Ala	Leu	Ala	Phe	Thr	Gly	Val	Thr	Leu	Leu	Leu	Leu	Leu	
65			70			75			80							
tdg																243
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<210> 12
<211> 80
<212> PRT
<213> Homo sapiens
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<400> 12
Met Ala Ala Pro Lys Gly Leu Leu Leu Val Ala Leu Val Leu Leu Leu
1 5 10 15

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<210> 13
<211> 555
<212> DNA
<213> Homo sapiens
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<400> 13

ctg gat ggc ggt acc act gcc ccc gcc ctc ctg ctc ctg ctg ctg ctg 96
Leu Asp Gly Gly Thr Thr Ala Pro Ala Leu Leu Leu Leu Leu Leu Leu
20 25 30

ctg ctt ttt gca ggc acc ccc acc acc cct gag tca atc caa gaa act 144
Leu Leu Phe Ala Gly Thr Pro Thr Thr Pro Glu Ser Ile Gln Glu Thr
35 40 45

gag gtc atc aac cca gga ccg cct agg ggc caa act tct cca gat ccc 192
Glu Val Ile Asn Pro Gly Pro Pro Arg Gly Gln Thr Ser Pro Asp Pro
50 55 60

tac tgg aag act ctg gat ggc agg gcc tgg gaa cct ggt ccc act gaa 240
Tyr Trp Lys Thr Leu Asp Gly Arg Ala Trp Glu Pro Gly Pro Thr Glu
65 70 75 80

acc aag gaa ctg gag gac aac gag gtc atc ccc agg agg atc tca ctc 288
Thr Lys Glu Leu Glu Asp Asn Glu Val Ile Pro Arg Arg Ile Ser Leu
85 90 95

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ttc tat gag cac tgg ttt gga ctt tag      555
Phe Tyr Glu His Trp Phe Gly Leu  *
          180

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<210> 14
<211> 184
<212> PRT
<213> Homo sapiens
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<400> 14															
Met	Thr	His	Tyr	Phe	Arg	Glu	Thr	Gln	Glu	Glu	Gly	Cys	Ser	Pro	Ser
1				5				10						15	
Leu	Asp	Gly	Gly	Thr	Thr	Ala	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Leu	Leu
			20					25						30	
Leu	Leu	Phe	Ala	Gly	Thr	Pro	Thr	Thr	Pro	Glu	Ser	Ile	Gln	Glu	Thr
		35					40					45			
Glu	Val	Ile	Asn	Pro	Gly	Pro	Pro	Arg	Gly	Gln	Thr	Ser	Pro	Asp	Pro
	50					55					60				
Tyr	Trp	Lys	Thr	Leu	Asp	Gly	Arg	Ala	Trp	Glu	Pro	Gly	Pro	Thr	Glu
65					70					75					80
Thr	Lys	Glu	Leu	Glu	Asp	Asn	Glu	Val	Ile	Pro	Arg	Arg	Ile	Ser	Leu
				85					90					95	

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<210> 15
<211> 567
<212> DNA
<213> Homo sapiens
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<220>
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<222> (1)...(567)

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Met	Gln	Gly	Ser	Ala	Leu	Pro	Gly	Thr	Trp	Leu	Gln	Ala	Leu	Leu	Val	
1			5			10			15							
tgg	ctg	gcc	tgg	gcc	ccg	gct	gcc	tct	gcc	tac	agt	gcc	atc	cac	gct	96
Trp	Leu	Ala	Trp	Ala	Pro	Ala	Ala	Ser	Ala	Tyr	Ser	Ala	Ile	His	Ala	
			20			25			30							
agg	gaa	cag	ctg	tcc	cca	caa	gaa	cca	tgt	ggt	cca	tgt	ctg	ggc	agt	144
Arg	Glu	Gln	Leu	Ser	Pro	Gln	Glu	Pro	Cys	Gly	Pro	Cys	Leu	Gly	Ser	
35			40			45										
gac	cgc	ctc	act	tgc	agc	caa	ccc	cac	act	ctt	cag	tgg	tgc	cga	ggt	192
Asp	Arg	Leu	Thr	Cys	Ser	Gln	Pro	His	Thr	Leu	Gln	Trp	Cys	Arg	Gly	
50			55			60										
cct	gtg	gca	gac	tca	gcc	aat	ccc	agt	gtg	gac	ttg	act	cgg	tct	tgg	240
Pro	Val	Ala	Asp	Ser	Ala	Asn	Pro	Ser	Val	Asp	Leu	Thr	Arg	Ser	Trp	
65			70			75			80							


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<210> 17
<211> 474
<212> DNA
<213> Homo sapiens

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<221> CDS
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Met	Arg	Leu	Trp	Phe	Thr	Ala	Val	Leu	Thr	Ser	Trp	Ala	Gln	Ala	Ile	
1		5			10					15						
ctc	cct	tct	tgg	cct	ccc	aat	gtg	gtg	gta	tta	cag	gcc	ggg	cct	cca	96
Leu	Pro	Ser	Trp	Pro	Pro	Asn	Val	Val	Val	Leu	Gln	Ala	Gly	Pro	Pro	
			20		25					30						
ctt	tct	cat	gtc	acc	cac	tct	gct	att	act	cca	tgc	tcc	cat	cct	tcc	144
Leu	Ser	His	Val	Thr	His	Ser	Ala	Ile	Thr	Pro	Cys	Ser	His	Pro	Ser	
35			40					45								
tac	gtc	ctt	act	ttc	acc	cag	gat	gag	aaa	gtg	ccc	cac	cgt	gtc	cag	192
Tyr	Val	Leu	Thr	Phe	Thr	Gln	Asp	Glu	Lys	Val	Pro	His	Arg	Val	Gln	
50		55					60									

Cys Ala Gly Lys Ala Asp Leu Thr Leu His Val Asp Gly Val Thr Val
 100 105 110
 Leu Asn Val Gly Lys Glu Ser Leu Ser Ser Gln Leu Arg Gln Gln Lys
 115 120 125
 Pro Glu Thr Gly Ala Lys Lys Lys Asp Pro Ala Gly Leu Gly Trp Lys
 130 135 140
 Val Leu Asp Ala Gln Leu Phe Thr Pro Thr Gln Cys Met
 145 150 155

<210> 19
 <211> 495
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(495)

<400> 19

atg caa agg tgg aca ctg tgg gct gca gcc ttc ctg acc ctc cac tct 48
 Met Gln Arg Trp Thr Leu Trp Ala Ala Ala Phe Leu Thr Leu His Ser
 1 5 10 15

gca cag gcc ttt cca caa aca gac atc agt atc agt cca gcc ctg cca 96
 Ala Gln Ala Phe Pro Gln Thr Asp Ile Ser Ile Ser Pro Ala Leu Pro
 20 25 30

gag ctg ccc ctg cct tcc ctg tgc ccc ctg ttc tgg atg gag ttc aaa 144
 Glu Leu Pro Leu Pro Ser Leu Cys Pro Leu Phe Trp Met Glu Phe Lys
 35 40 45

ggc cac tgc tat cga ttc ttc cct ctc aat aag acc tgg gct gag gcc 192
 Gly His Cys Tyr Arg Phe Phe Pro Leu Asn Lys Thr Trp Ala Glu Ala
 50 55 60

gac ctc tac tgt tct gag ttc tct gtg ggc agg aag tcc gcc aag ctg 240
 Asp Leu Tyr Cys Ser Glu Phe Ser Val Gly Arg Lys Ser Ala Lys Leu
 65 70 75 80

gcc tcc atc cac agc tgg gag gag aat gtc ttt gta tat gac ctc gtg 288
 Ala Ser Ile His Ser Trp Glu Glu Asn Val Phe Val Tyr Asp Leu Val
 85 90 95

Met	Gln	Arg	Trp	Thr	Leu	Trp	Ala	Ala	Ala	Phe	Leu	Thr	Leu	His	Ser
1				5				10						15	
Ala	Gln	Ala	Phe	Pro	Gln	Thr	Asp	Ile	Ser	Ile	Ser	Pro	Ala	Leu	Pro
			20					25					30		
Glu	Leu	Pro	Leu	Pro	Ser	Leu	Cys	Pro	Leu	Phe	Trp	Met	Glu	Phe	Lys
		35					40					45			
Gly	His	Cys	Tyr	Arg	Phe	Phe	Pro	Leu	Asn	Lys	Thr	Trp	Ala	Glu	Ala
	50					55					60				
Asp	Leu	Tyr	Cys	Ser	Glu	Phe	Ser	Val	Gly	Arg	Lys	Ser	Ala	Lys	Leu
65					70					75					80
Ala	Ser	Ile	His	Ser	Trp	Glu	Glu	Asn	Val	Phe	Val	Tyr	Asp	Leu	Val
				85					90					95	
Asn	Ser	Cys	Val	Pro	Gly	Ile	Pro	Ala	Asp	Val	Trp	Thr	Gly	Leu	His
			100					105					110		
Asp	His	Arg	Gln	Glu	Gly	Gln	Phe	Glu	Trp	Thr	Asp	Gly	Ser	Ser	Tyr
		115					120					125			

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<210> 21
<211> 531
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (1)...(531)

<400> 21																	
atg	ccc	agg	gtg	atg	gcc	tgg	agg	tac	tgg	gtc	cac	aca	gat	ggc	tgc		48
Met	Pro	Arg	Val	Met	Ala	Trp	Arg	Tyr	Trp	Val	His	Thr	Asp	Gly	Cys		
1				5					10					15			
tgc	agc	caa	ccc	tgc	cag	agt	ccc	caa	ggg	gcc	cta	gcc	atg	ctg	ccg		96
Cys	Ser	Gln	Pro	Cys	Gln	Ser	Pro	Gln	Gly	Ala	Leu	Ala	Met	Leu	Pro		
			20					25					30				
ctt	gtg	cta	gcc	ttc	atc	agt	gaa	atc	tca	gcc	caa	cca	aac	cag	ttt		144
Leu	Val	Leu	Ala	Phe	Ile	Ser	Glu	Ile	Ser	Ala	Gln	Pro	Asn	Gln	Phe		
		35					40					45					
cag	ggg	gcc	agc	tca	gtg	aca	ttc	att	tcc	aca	ctt	ttg	ttg	aac	ccg		192
Gln	Gly	Ala	Ser	Ser	Val	Thr	Phe	Ile	Ser	Thr	Leu	Leu	Leu	Asn	Pro		
	50					55					60						
acc	ttc	act	aag	cac	tgg	ctc	tgc	acc	agg	agt	gtg	cgg	ggc	cct	ggc		240
Thr	Phe	Thr	Lys	His	Trp	Leu	Cys	Thr	Arg	Ser	Val	Arg	Gly	Pro	Gly		
65					70				75						80		
atg	cag	ggg	ccc	cag	gcc	agc	ccc	agc	cct	gct	ctg	gag	ctt	atg	atg		288
Met	Gln	Gly	Pro	Gln	Ala	Ser	Pro	Ser	Pro	Ala	Leu	Glu	Leu	Met	Met		
				85					90					95			
gaa	ctt	aac	cag	aag	aag	cta	agg	aag	aga	aga	gag	gag	agg	aga	gag		336
Glu	Leu	Asn	Gln	Lys	Lys	Leu	Arg	Lys	Arg	Arg	Glu	Glu	Arg	Arg	Glu		

<210> 24
 <211> 93
 <212> PRT
 <213> Homo sapiens

<400> 24
 Met Ala Arg Cys Pro Leu Leu Leu Phe Pro Leu Pro Leu Val Pro Met
 1 5 10 15
 Ala Leu Gly Ala Ser Ala Gly Gly Arg His Ala Phe Gly Tyr Arg His
 20 25 30
 Met Phe Leu Gln Glu Glu Trp Trp Lys Gly Gly Ile Leu Trp Pro Pro
 35 40 45
 Thr Leu Glu Glu Gly Ser Met Trp Glu Glu Thr Ala His Arg Ser Ser
 50 55 60
 Met Arg His Arg Arg Glu Pro Leu Gly Val Val Ala Asp Glu Ala Val
 65 70 75 80
 Pro Pro Arg Val Leu Met Gly Thr Pro Gly His Glu Glu
 85 90

<210> 25
 <211> 372
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(372)

<400> 25
 atg ccc cct gac ccc aag gca ctg ctc tgc ctc aac ctc ccc cac ttc 48
 Met Pro Pro Asp Pro Lys Ala Leu Leu Cys Leu Asn Leu Pro His Phe
 1 5 10 15
 gcc ctg tgc cag ccc tgg gta ccc tcc ctg cag gcc gcg tcc ctc gcc 96
 Ala Leu Cys Gln Pro Trp Val Pro Ser Leu Gln Ala Ala Ser Leu Ala
 20 25 30
 acc tgg cct cct gtc ttc tgg aac tca ggc cct gcc ccc tgc tcc cag 144
 Thr Trp Pro Pro Val Phe Trp Asn Ser Gly Pro Ala Pro Cys Ser Gln
 35 40 45
 cct cca atg ccc acg tcc aac agg act ctg ctt ctc agc ccc acc tca 192

Met	Glu	Thr	Glu	Pro	Ser	Lys	Ala	Arg	Ala	Asn	Asp	Pro	Gly	Ser	Ala
1				5					10					15	
Ala	Glu	Gly	Leu	Ser	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Val	Gln	Ala
			20					25					30		
Gly	Val	Trp	Gly	Phe	Pro	Arg	Pro	Pro	Gly	Arg	Pro	Gln	Leu	Ser	Leu
		35					40					45			
Gln	Glu	Leu	Arg	Arg	Glu	Phe	Thr	Val	Ser	Leu	His	Leu	Ala	Arg	Lys
	50					55					60				
Leu	Leu	Ser	Glu	Val	Arg	Gly	Gln	Ala	His	Arg	Phe	Asp	Pro	Glu	Arg
65					70					75				80	
Leu	Cys	Phe	Ile	Ser	Thr	Thr	Leu	Gln	Pro	Phe	His	Ala	Leu	Leu	Gly
				85					90					95	
Gly	Leu	Gly	Thr	Gln	Gly	Arg	Trp	Thr	Asn	Met	Glu	Arg	Met	Gln	Leu

100 105 110
 Trp Ala Met Arg Leu Asp Leu Arg Asp Leu Gln Arg His Leu Arg Phe
 115 120 125
 Gln Val Leu Ala Ala Gly Phe Asn Leu Pro Glu Glu Glu Glu Glu Glu
 130 135 140
 Glu Glu Glu Glu Glu Glu Glu Arg Lys Gly Leu Leu Pro Gly Ala Leu
 145 150 155 160
 Gly Ser Ala Leu Gln Gly Pro Ala Gln Val Ser Trp Pro Gln Leu Leu
 165 170 175
 Ser Thr Tyr Arg Leu Leu His Ser Leu Glu Leu Val Leu Ser Arg Ala
 180 185 190
 Val Arg Glu Leu Leu Leu Leu Ser Lys Ala Gly His Ser Val Trp Pro
 195 200 205
 Leu Gly Phe Pro Thr Leu Ser Pro Gln Pro
 210 215

<210> 29
 <211> 533
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(533)

<400> 29

atg cac gtt cca gtg ata aag ctg tgc acg gca gcc atg gct atc cag 48
 Met His Val Pro Val Ile Lys Leu Cys Thr Ala Ala Met Ala Ile Gln
 1 5 10 15

ctg gcc cag ccc aac aga gat ctg tgg ttc ctc act tgc ctg cac ctt 96
 Leu Ala Gln Pro Asn Arg Asp Leu Trp Phe Leu Thr Cys Leu His Leu
 20 25 30

ctc tgc ctt ctc ctc tta cca tca cct cca ata tca gca ggt cct ggt 144
 Leu Cys Leu Leu Leu Leu Pro Ser Pro Pro Ile Ser Ala Gly Pro Gly
 35 40 45

cct tct ctg cct tct ccc ctc acc atc atg tcc aat atc agc agc tgc 192
 Pro Ser Leu Pro Ser Pro Leu Thr Ile Met Ser Asn Ile Ser Ser Cys
 50 55 60

cag agc ctg gcc cca cca tca tcc tct ccc agc tgg aca ggt gtt cct 240

Gln Ser Leu Ala Pro Pro Ser Ser Ser Pro Ser Trp Thr Gly Val Pro
 65 70 75 80
 gcc ttc caa gta ggg tcc cag cct cca ccc ttg gag gta gac cta cag 288
 Ala Phe Gln Val Gly Ser Gln Pro Pro Pro Leu Glu Val Asp Leu Gln
 85 90 95
 gaa ctc ttc gga gag gac aag cgc ctt tta aag gtc gag cat cta tgc 336
 Glu Leu Phe Gly Glu Asp Lys Arg Leu Leu Lys Val Glu His Leu Cys
 100 105 110
 tgc tgc ggc tac gta cct gtc acg agc atc caa cca att tgg ggc gcg 384
 Cys Cys Gly Tyr Val Pro Val Thr Ser Ile Gln Pro Ile Trp Gly Ala
 115 120 125
 cat ctg ctg tgc tta aag ggc aag ttc aac act gtt aag ttt gtg ttg 432
 His Leu Leu Cys Leu Lys Gly Lys Phe Asn Thr Val Lys Phe Val Leu
 130 135 140
 caa cga agc cag att gtg tgg gca caa tcc agt acc agg ggt ctg act 480
 Gln Arg Ser Gln Ile Val Trp Ala Gln Ser Ser Thr Arg Gly Leu Thr
 145 150 155 160
 act aac agt cgc ata tta cct ccc tta tac ctc ccg tgt atg ctc cta 528
 Thr Asn Ser Arg Ile Leu Pro Pro Leu Tyr Leu Pro Cys Met Leu Leu
 165 170 175
 gcc cg 533
 Ala

<210> 30
 <211> 177
 <212> PRT
 <213> Homo sapiens

<400> 30
 Met His Val Pro Val Ile Lys Leu Cys Thr Ala Ala Met Ala Ile Gln
 1 5 10 15
 Leu Ala Gln Pro Asn Arg Asp Leu Trp Phe Leu Thr Cys Leu His Leu
 20 25 30
 Leu Cys Leu Leu Leu Leu Pro Ser Pro Pro Ile Ser Ala Gly Pro Gly

35 40 45
 Pro Ser Leu Pro Ser Pro Leu Thr Ile Met Ser Asn Ile Ser Ser Cys
 50 55 60
 Gln Ser Leu Ala Pro Pro Ser Ser Ser Pro Ser Trp Thr Gly Val Pro
 65 70 75 80
 Ala Phe Gln Val Gly Ser Gln Pro Pro Pro Leu Glu Val Asp Leu Gln
 85 90 95
 Glu Leu Phe Gly Glu Asp Lys Arg Leu Leu Lys Val Glu His Leu Cys
 100 105 110
 Cys Cys Gly Tyr Val Pro Val Thr Ser Ile Gln Pro Ile Trp Gly Ala
 115 120 125
 His Leu Leu Cys Leu Lys Gly Lys Phe Asn Thr Val Lys Phe Val Leu
 130 135 140
 Gln Arg Ser Gln Ile Val Trp Ala Gln Ser Ser Thr Arg Gly Leu Thr
 145 150 155 160
 Thr Asn Ser Arg Ile Leu Pro Pro Leu Tyr Leu Pro Cys Met Leu Leu
 165 170 175
 Ala

<210> 31
 <211> 525
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(525)

<400> 31
 atg gga gtc tca ctg gat cag gag cac agc aga cac cct gct gga tct 48
 Met Gly Val Ser Leu Asp Gln Glu His Ser Arg His Pro Ala Gly Ser
 1 5 10 15
 gga ggt atg gga gtc agc ggc agg tct gcg aca gtg gca aac agc agt 96
 Gly Gly Met Gly Val Ser Gly Arg Ser Ala Thr Val Ala Asn Ser Ser
 20 25 30
 ggt gga tgg atc ttt ggg gtg ttg ctt ttc tca ccg gaa acc tct gca 144
 Gly Gly Trp Ile Phe Gly Val Leu Leu Phe Ser Pro Glu Thr Ser Ala
 35 40 45
 gcc agt ggc atc ttt gcc caa gtt cat gtc ctg tgt cca gga aga atg 192

35 40 45
 Ala Ser Gly Ile Phe Ala Gln Val His Val Leu Cys Pro Gly Arg Met
 50 55 60
 Arg Tyr Ala Asp Lys Trp Arg Arg Glu Gly Ser Ala Cys Arg Leu Val
 65 70 75 80
 His Arg Gln Pro Trp Ala Ala Gly Lys Gly Thr Thr Ser Pro His Ser
 85 90 95
 Gly Gln Trp Asn Ser Ser Pro Thr Pro Ser Leu Gln Asp Leu Pro Gly
 100 105 110
 Leu Lys Asn Arg Asn Leu Ala Ala Met Lys Leu Asp Lys Pro Ile Pro
 115 120 125
 Ser Pro Ser Leu Arg His Asn Leu Phe Glu Ile Leu Arg Ala Arg Gln
 130 135 140
 Pro Cys Leu Tyr Ala Cys Asn Ser Lys Leu Arg Ile Arg Gly Pro Ala
 145 150 155 160
 Gly Pro Leu Glu Ser Met Gly Leu Arg Cys Arg Ser Pro Glu
 165 170

<210> 33
 <211> 369
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(369)

<400> 33
 atg cgc tcc ctg cat aac gcg cgg cac gcc tcc ttc gct caa ctt ggc 48
 Met Arg Ser Leu His Asn Ala Arg His Ala Ser Phe Ala Gln Leu Gly
 1 5 10 15
 cgt atg ttg att gtc agc atc aac aag ctc cta atg cca cct tta aaa 96
 Arg Met Leu Ile Val Ser Ile Asn Lys Leu Leu Met Pro Pro Leu Lys
 20 25 30
 gtg tct ata tct ctt tta aga tta tta cct cct aca ttt gct gtg ctc 144
 Val Ser Ile Ser Leu Leu Arg Leu Leu Pro Pro Thr Phe Ala Val Leu
 35 40 45
 ttt gta tac aac tcc cgt ttc cgc gct gct tct tac atg caa cac ctc 192
 Phe Val Tyr Asn Ser Arg Phe Arg Ala Ala Ser Tyr Met Gln His Leu
 50 55 60

<210> 35
<211> 1148

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1148)

<400> 35

atg	gag	ccc	ctg	cgc	gcg	ccc	gcg	ctg	cgc	cgc	ctg	ctg	ccg	ccg	ctg	48
Met	Glu	Pro	Leu	Arg	Ala	Pro	Ala	Leu	Arg	Arg	Leu	Leu	Pro	Pro	Leu	
1				5					10					15		

ctg	ctc	ctg	ctg	ctg	tca	ctg	ccc	ccc	cgc	gcc	cgg	gcc	aag	tac	gtg	96
Leu	Leu	Leu	Leu	Leu	Ser	Leu	Pro	Pro	Arg	Ala	Arg	Ala	Lys	Tyr	Val	
			20					25					30			

cgg	ggc	aac	ctc	agt	tcc	aag	gag	gac	tgg	gtg	ttc	ctg	aca	aga	ttt	144
Arg	Gly	Asn	Leu	Ser	Ser	Lys	Glu	Asp	Trp	Val	Phe	Leu	Thr	Arg	Phe	
		35					40					45				

tgt	ttc	ctc	tcg	gat	tac	ggc	cga	ctg	gac	ttc	cgt	ttc	cgc	tac	cct	192
Cys	Phe	Leu	Ser	Asp	Tyr	Gly	Arg	Leu	Asp	Phe	Arg	Phe	Arg	Tyr	Pro	
	50					55				60						

gag	gcc	aag	tgc	tgt	cag	aac	atc	ctc	ctc	tat	ttt	gat	gac	cca	tcc	240
Glu	Ala	Lys	Cys	Cys	Gln	Asn	Ile	Leu	Leu	Tyr	Phe	Asp	Asp	Pro	Ser	
65					70					75					80	

cag	tgg	cca	gcc	gtg	tac	aag	gca	ggg	gac	aag	gac	tgc	ctg	gcc	aag	288
Gln	Trp	Pro	Ala	Val	Tyr	Lys	Ala	Gly	Asp	Lys	Asp	Cys	Leu	Ala	Lys	
				85					90					95		

gag	tca	gtg	atc	cgg	ccg	gag	aac	aac	cag	gtc	atc	aac	ctc	acc	acc	336
Glu	Ser	Val	Ile	Arg	Pro	Glu	Asn	Asn	Gln	Val	Ile	Asn	Leu	Thr	Thr	
			100					105					110			

cag	tat	gcc	tgg	tcc	ggc	tgt	cag	gtg	gta	tca	gag	gag	gga	acc	cgc	384
Gln	Tyr	Ala	Trp	Ser	Gly	Cys	Gln	Val	Val	Ser	Glu	Glu	Gly	Thr	Arg	
		115				120						125				

tac	ctg	agc	tgc	tcc	agt	ggc	cgc	agc	ttc	cgc	tca	gtg	cgt	gaa	cgg	432
Tyr	Leu	Ser	Cys	Ser	Ser	Gly	Arg	Ser	Phe	Arg	Ser	Val	Arg	Glu	Arg	
	130					135					140					

tgg tgg tat att gcg ctc agc aag tgt ggg ggt gat gga ttg cag ctg	480
Trp Trp Tyr Ile Ala Leu Ser Lys Cys Gly Gly Asp Gly Leu Gln Leu	
145 150 155 160	
gag tat gag atg gtc ctc acc aat ggc aag tcc ttc tgg aca cga cac	528
Glu Tyr Glu Met Val Leu Thr Asn Gly Lys Ser Phe Trp Thr Arg His	
165 170 175	
ttc tcc gct gat gag ttt ggg atc ctg gag aca gat gtg acc ttc ctc	576
Phe Ser Ala Asp Glu Phe Gly Ile Leu Glu Thr Asp Val Thr Phe Leu	
180 185 190	
ctc atc ttc atc ctc atc ttc ttc ctc tct tgt tac ttt gga tat ttg	624
Leu Ile Phe Ile Leu Ile Phe Phe Leu Ser Cys Tyr Phe Gly Tyr Leu	
195 200 205	
ctg aaa ggt cgt cag ttg ctc cac aca act tat aaa atg ttc atg gcc	672
Leu Lys Gly Arg Gln Leu Leu His Thr Thr Tyr Lys Met Phe Met Ala	
210 215 220	
gca gca gga gta gag gtc ctg agc ctc cta ttt ttc tgc atc tac tgg	720
Ala Ala Gly Val Glu Val Leu Ser Leu Leu Phe Phe Cys Ile Tyr Trp	
225 230 235 240	
ggt caa tat gcc acc gat ggc att ggc aac gag agt gtg aag atc ttg	768
Gly Gln Tyr Ala Thr Asp Gly Ile Gly Asn Glu Ser Val Lys Ile Leu	
245 250 255	
gcc aag ctg ctc ttc tcc tcc agc ttc ctc atc ttc ctg ctg atg ctt	816
Ala Lys Leu Leu Phe Ser Ser Ser Phe Leu Ile Phe Leu Leu Met Leu	
260 265 270	
atc ctc ctg ggg aag gga ttc acg gtg aca cgg tgc ccg ggc agg gcg	864
Ile Leu Leu Gly Lys Gly Phe Thr Val Thr Arg Cys Pro Gly Arg Ala	
275 280 285	
tgc tcg tgg ggc ggc tgg ggc cgc atc agc cac gcg ggc tcc gtg aag	912
Cys Ser Trp Gly Gly Trp Gly Arg Ile Ser His Ala Gly Ser Val Lys	
290 295 300	
ttg tct gtc tac atg acc ctg tac acg ctc acc cat gtg gtg ctg ctc	960
Leu Ser Val Tyr Met Thr Leu Tyr Thr Leu Thr His Val Val Leu Leu	

305	310	315	320	
atc tac gag gcg gaa ttc ttt gac cca ggc cag gta ctg tac acg tat				1008
Ile Tyr Glu Ala Glu Phe Phe Asp Pro Gly Gln Val Leu Tyr Thr Tyr				
	325	330	335	
gag tcg ccg gcc ggc tac ggg ctc att gga ctg cag gtg gcg gcc tac				1056
Glu Ser Pro Ala Gly Tyr Gly Leu Ile Gly Leu Gln Val Ala Ala Tyr				
	340	345	350	
gtg tgg ttc tgc tat gct gtg ctt gtc tca ctg cga cac ttt cct gag				1104
Val Trp Phe Cys Tyr Ala Val Leu Val Ser Leu Arg His Phe Pro Glu				
	355	360	365	
aag cag cct ttt tat gtg ccc ttc ttt gct gcc tat acc ctc tg				1148
Lys Gln Pro Phe Tyr Val Pro Phe Phe Ala Ala Tyr Thr Leu				
	370	375	380	

<210> 36

<211> 382

<212> PRT

<213> Homo sapiens

<400> 36

Met Glu Pro Leu Arg Ala Pro Ala Leu Arg Arg Leu Leu Pro Pro Leu			
1 5 10 15			
Leu Leu Leu Leu Leu Ser Leu Pro Pro Arg Ala Arg Ala Lys Tyr Val			
20 25 30			
Arg Gly Asn Leu Ser Ser Lys Glu Asp Trp Val Phe Leu Thr Arg Phe			
35 40 45			
Cys Phe Leu Ser Asp Tyr Gly Arg Leu Asp Phe Arg Phe Arg Tyr Pro			
50 55 60			
Glu Ala Lys Cys Cys Gln Asn Ile Leu Leu Tyr Phe Asp Asp Pro Ser			
65 70 75 80			
Gln Trp Pro Ala Val Tyr Lys Ala Gly Asp Lys Asp Cys Leu Ala Lys			
85 90 95			
Glu Ser Val Ile Arg Pro Glu Asn Asn Gln Val Ile Asn Leu Thr Thr			
100 105 110			
Gln Tyr Ala Trp Ser Gly Cys Gln Val Val Ser Glu Glu Gly Thr Arg			
115 120 125			
Tyr Leu Ser Cys Ser Ser Gly Arg Ser Phe Arg Ser Val Arg Glu Arg			
130 135 140			

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1	5	10	15	
ctg ata ctt cct ctg ctg ctc ttc tgg tgc ttg agc ggg tct agt cgt				96
Leu Ile Leu Pro Leu Leu Leu Phe Trp Ser Leu Ser Gly Ser Ser Arg				
	20	25	30	
gct act gtc gct act gga cgg tgc cgt agt cgt cgt ata gtg cgt cgt				144
Ala Thr Val Ala Thr Gly Arg Ser Arg Ser Arg Arg Ile Val Arg Arg				
	35	40	45	
gga cct cat gga gat gat agc tac gtg ctt ccg atc gtc gta gat aaa				192
Gly Pro His Gly Asp Asp Ser Tyr Val Leu Pro Ile Val Val Asp Lys				
	50	55	60	
tgg ttg ggc cgt tca ctg acc gtc atc ctc aag cac ggg cta cgg cgg				240
Trp Leu Gly Arg Ser Leu Thr Val Ile Leu Lys His Gly Leu Arg Arg				
	65	70	75	80
ctc gtc gag gac gat aag cac ccg ccc ctc ctc tgg gga tat gtg gct				288
Leu Val Glu Asp Asp Lys His Pro Pro Leu Leu Trp Gly Tyr Val Ala				
	85	90	95	
cca gtg tgg ggg ggc ccc agt gac cca ttt gtt gaa atg ata taa				333
Pro Val Trp Gly Gly Pro Ser Asp Pro Phe Val Glu Met Ile *				
	100	105	110	

<210> 38

<211> 110

<212> PRT

<213> Homo sapiens

<400> 38

Met Ser Val Val Glu Val Gln Gly Leu Val Cys Tyr Ala Arg Arg Pro				
1	5	10	15	
Leu Ile Leu Pro Leu Leu Leu Phe Trp Ser Leu Ser Gly Ser Ser Arg				
	20	25	30	
Ala Thr Val Ala Thr Gly Arg Ser Arg Ser Arg Arg Ile Val Arg Arg				
	35	40	45	
Gly Pro His Gly Asp Asp Ser Tyr Val Leu Pro Ile Val Val Asp Lys				
	50	55	60	
Trp Leu Gly Arg Ser Leu Thr Val Ile Leu Lys His Gly Leu Arg Arg				
	65	70	75	80

cat ggt tcc cct gca gcc acc tct gac tct cgg cag tgg gca gct agg 384
 His Gly Ser Pro Ala Ala Thr Ser Asp Ser Arg Gln Trp Ala Ala Arg
 115 120 125

act tcc ctc gag ggg ctg gct gag ctc ctt ggt gct caa tgt cgt acc 432
 Thr Ser Leu Glu Gly Leu Ala Glu Leu Leu Gly Ala Gln Cys Arg Thr
 130 135 140

att tac tga 441
 Ile Tyr *
 145

<210> 40
 <211> 146
 <212> PRT
 <213> Homo sapiens

<400> 40
 Leu Gln Ser Tyr Arg Ser Asn Cys Gln Leu Asp Lys Pro Asn Ser Ser
 1 5 10 15
 Pro Ala Met Ala Pro Pro Asp Gly Ala Ala Leu Leu Leu Leu Leu Leu
 20 25 30
 Leu Phe Thr Ala Ala Ser Ile Lys Thr Ala Asn Ser Ile Gly Ser Pro
 35 40 45
 Leu Pro Ser Phe Leu Gly Glu Ala Thr Asn Pro Pro Gly Arg His Val
 50 55 60
 Lys Arg Tyr Gly His Phe Glu Glu Gln Leu Gly His Phe Leu Lys Ser
 65 70 75 80
 Glu Thr Tyr Tyr Met Thr Gln Ser Phe Cys Ser Tyr Ala Pro Pro Gln
 85 90 95
 Gln Gln Cys Gly Gln Gly Ala Gln Asp Glu Cys Glu Lys Glu Gly Cys
 100 105 110
 His Gly Ser Pro Ala Ala Thr Ser Asp Ser Arg Gln Trp Ala Ala Arg
 115 120 125
 Thr Ser Leu Glu Gly Leu Ala Glu Leu Leu Gly Ala Gln Cys Arg Thr
 130 135 140
 Ile Tyr
 145

<210> 41
 <211> 441
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(441)

<400> 41

atg ctg ttg ctg cag ctg ctg ctg ctg ctg ccg ccg ctg ctg ctc ctg	48
Met Leu Leu Leu Gln Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu Leu	
1 5 10 15	
ctt ttt tca gtc tca ctc tgt tgc cca ggc tgg agt gaa gtg ggc atg	96
Leu Phe Ser Val Ser Leu Cys Cys Pro Gly Trp Ser Glu Val Gly Met	
20 25 30	
gaa gtc aaa cca ggt ctc cct tcc cac aac tcg ctg ccc cag ccc atg	144
Glu Val Lys Pro Gly Leu Pro Ser His Asn Ser Leu Pro Gln Pro Met	
35 40 45	
gca gat gga cat ccc cca agg gca tta caa cca tgg cac aag gac acc	192
Ala Asp Gly His Pro Pro Arg Ala Leu Gln Pro Trp His Lys Asp Thr	
50 55 60	
ctt ggt cca gag gga agt tgc aaa gtc tgg ttt gcc tgg aag gag ctc	240
Leu Gly Pro Glu Gly Ser Cys Lys Val Trp Phe Ala Trp Lys Glu Leu	
65 70 75 80	
ttc cag gtg gag gaa gcg gca gat aaa gaa act gaa gtt cag agt gtc	288
Phe Gln Val Glu Glu Ala Ala Asp Lys Glu Thr Glu Val Gln Ser Val	
85 90 95	
agc tta ccc aag gtc aca tct gaa aag cag cag aga cag gtt tca acc	336
Ser Leu Pro Lys Val Thr Ser Glu Lys Gln Gln Arg Gln Val Ser Thr	
100 105 110	
cag att ggg ctg act cca agc ccc atg ctg att ccc tgt ggc acc tgc	384
Gln Ile Gly Leu Thr Pro Ser Pro Met Leu Ile Pro Cys Gly Thr Cys	
115 120 125	
ctc tcg gct ggt aca gaa aac cag gga aag ctg tat ttg aat ctc aac	432
Leu Ser Ala Gly Thr Glu Asn Gln Gly Lys Leu Tyr Leu Asn Leu Asn	
130 135 140	

cca atc tga
Pro Ile *
145

441

<210> 42
<211> 146
<212> PRT
<213> Homo sapiens

<400> 42

Met Leu Leu Leu Gln Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu Leu
1 5 10 15
Leu Phe Ser Val Ser Leu Cys Cys Pro Gly Trp Ser Glu Val Gly Met
20 25 30
Glu Val Lys Pro Gly Leu Pro Ser His Asn Ser Leu Pro Gln Pro Met
35 40 45
Ala Asp Gly His Pro Pro Arg Ala Leu Gln Pro Trp His Lys Asp Thr
50 55 60
Leu Gly Pro Glu Gly Ser Cys Lys Val Trp Phe Ala Trp Lys Glu Leu
65 70 75 80
Phe Gln Val Glu Glu Ala Ala Asp Lys Glu Thr Glu Val Gln Ser Val
85 90 95
Ser Leu Pro Lys Val Thr Ser Glu Lys Gln Gln Arg Gln Val Ser Thr
100 105 110
Gln Ile Gly Leu Thr Pro Ser Pro Met Leu Ile Pro Cys Gly Thr Cys
115 120 125
Leu Ser Ala Gly Thr Glu Asn Gln Gly Lys Leu Tyr Leu Asn Leu Asn
130 135 140
Pro Ile
145

<210> 43
<211> 203
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(203)

<400> 43

atg act ggc tgt ccg gcg tca tca aga cgc cga ggc ttc ggg ctc ttt

48

<210> 46
 <211> 146
 <212> PRT
 <213> Homo sapiens

<400> 46
 Met Ala Leu Ser Trp Leu Ala Leu Ser Pro Gly Leu Gln Gly Gln Asn
 1 5 10 15
 Leu Leu Glu Ala Gly Arg Arg Thr Ser Gln Ile Pro Pro Gly Ser Leu
 20 25 30
 Arg Asp Tyr Thr Val Pro Leu Cys Arg Leu Glu Pro Arg Pro Ala Phe
 35 40 45
 Ser Val Ala Ala Leu Ala Leu Arg Ala Thr Ser Leu Ala Ala Gln Gly
 50 55 60
 Tyr Glu Glu Gly Met Glu Asp Lys Asp Asn Ser Gly Asn Arg Glu Asp
 65 70 75 80
 Gly Ser Thr Asp Ser Val Thr Trp Gly Phe Glu Lys Gly Asp Arg Tyr
 85 90 95
 Trp Leu Pro Leu Arg Ser Cys Gly Ile Met Met Leu Glu Gln Val Ser
 100 105 110
 Thr Phe Ile His Met Gln Glu Asp Phe Asp Gln Val Leu Thr Val Asn
 115 120 125
 Met Glu Glu Lys Ser Pro Leu Ala Ser Ser Arg Gly Lys Glu Lys Glu
 130 135 140
 Thr Thr
 145

<210> 47
 <211> 384
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(384)

<400> 47
 atg gta aag ctg ctg ctc tcc ctg ctg tcc aca act ggg gcc tgg agc
 Met Val Lys Leu Leu Leu Ser Leu Leu Ser Thr Thr Gly Ala Trp Ser
 1 5 10 15

Met	Val	Lys	Leu	Leu	Leu	Ser	Leu	Leu	Ser	Thr	Thr	Gly	Ala	Trp	Ser
1				5					10					15	
Trp	Gly	His	Ile	Leu	Gln	Pro	Glu	Gly	Ser	Trp	Glu	Leu	Trp	Leu	Pro
			20					25					30		
Gly	Ser	Thr	Val	Ala	Pro	Thr	Asp	Leu	Gln	Trp	Val	Leu	His	Pro	Gly
		35					40					45			
Leu	Leu	Ser	Glu	Thr	Asn	Thr	Leu	Pro	Ser	Phe	Leu	Leu	Gly	Thr	Val
	50					55					60				

Thr Thr Arg Thr Tyr Cys Ala Ser Gly Thr Val Gln Arg Leu Asp Ile
 65 70 75 80
 Ser Leu Leu Gln Pro Trp Gly Tyr Glu Lys Pro Cys Pro Ile Leu Ala
 85 90 95
 Glu Gly Ala Glu Val Gly Arg Arg Val Gly Thr Thr Glu Ser Arg Glu
 100 105 110
 Leu Asn Thr His Lys Glu Ser Lys Ile Cys Phe Tyr Ser Glu Ser
 115 120 125

<210> 49
 <211> 1110
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1110)

<400> 49

atg cca ccc atg ctg tgg ctg ctg ctc cac ttt gct gcc ccg gca ctg 48
 Met Pro Pro Met Leu Trp Leu Leu Leu His Phe Ala Ala Pro Ala Leu
 1 5 10 15

ggg ttc tac ttt tcc atc agc tgc ccc agt ggt aag cag tgc caa cag 96
 Gly Phe Tyr Phe Ser Ile Ser Cys Pro Ser Gly Lys Gln Cys Gln Gln
 20 25 30

gcc cta ctc tca ggc aat gat att ctc ctg tat tgc aac tcc tcg ggg 144
 Ala Leu Leu Ser Gly Asn Asp Ile Leu Leu Tyr Cys Asn Ser Ser Gly
 35 40 45

gcg cac tgg tac tat tta ttc aca caa ggc aag aag ggc agg ctc acc 192
 Ala His Trp Tyr Tyr Leu Phe Thr Gln Gly Lys Lys Gly Arg Leu Thr
 50 55 60

agc ctc acc aat att tcc aat atg gaa ata atg ccc gag ggc agc ctt 240
 Ser Leu Thr Asn Ile Ser Asn Met Glu Ile Met Pro Glu Gly Ser Leu
 65 70 75 80

ctc att aaa gat cca ttg ccc tcc cag acg ggc ctc tac cac tgc tgg 288
 Leu Ile Lys Asp Pro Leu Pro Ser Gln Thr Gly Leu Tyr His Cys Trp
 85 90 95

aac aag aat ggc cgc caa gtg gtg cag tat gaa att gac ttt cag gat	336
Asn Lys Asn Gly Arg Gln Val Val Gln Tyr Glu Ile Asp Phe Gln Asp	
100 105 110	
gtc acc acc ctg cat ata aca cac aag gac ctg ggt cag agg ccc ctg	384
Val Thr Thr Leu His Ile Thr His Lys Asp Leu Gly Gln Arg Pro Leu	
115 120 125	
cag aac gag acc ctg cat ttg ggc agc aaa cag ctc att ttt acc tgg	432
Gln Asn Glu Thr Leu His Leu Gly Ser Lys Gln Leu Ile Phe Thr Trp	
130 135 140	
tgg gag ccc tgg cag gac tgc aac cgc tgt gag gag ccg ggc gag tgt	480
Trp Glu Pro Trp Gln Asp Cys Asn Arg Cys Glu Glu Pro Gly Glu Cys	
145 150 155 160	
aaa cgc ctg ggg tac cgc tac att gag gag cct ctg gag gaa gcc atg	528
Lys Arg Leu Gly Tyr Arg Tyr Ile Glu Glu Pro Leu Glu Glu Ala Met	
165 170 175	
ccc tgc tgg ctc tat ctg gga gag gtg ctg gtg tgg tct agc cgc ttg	576
Pro Cys Trp Leu Tyr Leu Gly Glu Val Leu Val Trp Ser Ser Arg Leu	
180 185 190	
cgg cct gag ctg cag gtg gaa gcc tgc cac gtc cag tgc acc aat aac	624
Arg Pro Glu Leu Gln Val Glu Ala Cys His Val Gln Cys Thr Asn Asn	
195 200 205	
aca cag tta agg gtg gat tac gtc att ttt gac aac ttc agg ctc gat	672
Thr Gln Leu Arg Val Asp Tyr Val Ile Phe Asp Asn Phe Arg Leu Asp	
210 215 220	
gag aag aca gaa ttt gtg tgg ctc gac tgt ccc tta gga tcc atg tac	720
Glu Lys Thr Glu Phe Val Trp Leu Asp Cys Pro Leu Gly Ser Met Tyr	
225 230 235 240	
agg ccc gtc aac tgg cgt gcc aac gac acc ccc ctg acg tgg gag agc	768
Arg Pro Val Asn Trp Arg Ala Asn Asp Thr Pro Leu Thr Trp Glu Ser	
245 250 255	
cag ctc tcc ggc cag gac ttc acc acc ttt ctg gac ccc tcc acc ggc	816
Gln Leu Ser Gly Gln Asp Phe Thr Thr Phe Leu Asp Pro Ser Thr Gly	
260 265 270	

ggc agg cag ctg cag gtt ttc cag ccg gcc gtc tac aag tgc ttc gtg 864
 Gly Arg Gln Leu Gln Val Phe Gln Pro Ala Val Tyr Lys Cys Phe Val
 275 280 285

cag cag gag ctc gtg gcc cag ttc aaa ccc gcc gcc agt ctg gag acg 912
 Gln Gln Glu Leu Val Ala Gln Phe Lys Pro Ala Ala Ser Leu Glu Thr
 290 295 300

ctg gag gct cag tgg aga gag aac gat gcc cag tgg cgg gag gca agg 960
 Leu Glu Ala Gln Trp Arg Glu Asn Asp Ala Gln Trp Arg Glu Ala Arg
 305 310 315 320

aag gcc ctg cgg ggc agg gcg gac tcc gtg ctc aag ggg ctg aag ctg 1008
 Lys Ala Leu Arg Gly Arg Ala Asp Ser Val Leu Lys Gly Leu Lys Leu
 325 330 335

gtg ctg ctc gtg gtc acc gtc ctg gcc ctg ctg ggg gcg ctg ctc aag 1056
 Val Leu Leu Val Val Thr Val Leu Ala Leu Leu Gly Ala Leu Leu Lys
 340 345 350

tgc atc cac cct tcc ccg ggc agg aga agc aca cag gtg ctg gtg gtg 1104
 Cys Ile His Pro Ser Pro Gly Arg Arg Ser Thr Gln Val Leu Val Val
 355 360 365

aaa taa 1110
 Lys *

<210> 50

<211> 369

<212> PRT

<213> Homo sapiens

<400> 50

Met Pro Pro Met Leu Trp Leu Leu Leu His Phe Ala Ala Pro Ala Leu
 1 5 10 15
 Gly Phe Tyr Phe Ser Ile Ser Cys Pro Ser Gly Lys Gln Cys Gln Gln
 20 25 30
 Ala Leu Leu Ser Gly Asn Asp Ile Leu Leu Tyr Cys Asn Ser Ser Gly
 35 40 45
 Ala His Trp Tyr Tyr Leu Phe Thr Gln Gly Lys Lys Gly Arg Leu Thr

<210> 51

<211> 759
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(759)

<400> 51

atg gca gcc ccc gcc ctg ctg ctc cta gca ctg ctg ctg ccc gtg ggg	48
Met Ala Ala Pro Ala Leu Leu Leu Leu Ala Leu Leu Leu Pro Val Gly	
1 5 10 15	

gcc tgg ccc ggg ctg ccc agg agg ccc tgt gtg cac tgc tgc cgc ccg	96
Ala Trp Pro Gly Leu Pro Arg Arg Pro Cys Val His Cys Cys Arg Pro	
20 25 30	

gcc tgg ccc cct gga ccc tat gcc cgg gtg agt gac agg gac ctg tgg	144
Ala Trp Pro Pro Gly Pro Tyr Ala Arg Val Ser Asp Arg Asp Leu Trp	
35 40 45	

agg ggg gac ctg tgg agg ggg ctg cct cga gta cgg ccc act ata gac	192
Arg Gly Asp Leu Trp Arg Gly Leu Pro Arg Val Arg Pro Thr Ile Asp	
50 55 60	

atc gaa atc ctc aaa ggt gag aag ggt gag gcc ggc gtc cga ggt cgg	240
Ile Glu Ile Leu Lys Gly Glu Lys Gly Glu Ala Gly Val Arg Gly Arg	
65 70 75 80	

gcc ggc agg agc ggg aaa gag ggg ccg cca ggc gcc cgg ggc ctg cag	288
Ala Gly Arg Ser Gly Lys Glu Gly Pro Pro Gly Ala Arg Gly Leu Gln	
85 90 95	

ggc cgc aga ggc cag aag ggg cag gtg ggg ccg ccg ggc gcc gcg tgc	336
Gly Arg Arg Gly Gln Lys Gly Gln Val Gly Pro Pro Gly Ala Ala Cys	
100 105 110	

cga cgt gcc tac gcc gcc ttc tcc gtg ggc cgg cgc gag ggc ctg cac	384
Arg Arg Ala Tyr Ala Ala Phe Ser Val Gly Arg Arg Glu Gly Leu His	
115 120 125	

agc tcc gac cac ttc cag gcg gtg ccc ttc gac acg gag ctg gtg aac	432
Ser Ser Asp His Phe Gln Ala Val Pro Phe Asp Thr Glu Leu Val Asn	

130	135	140	
ctg gac ggc gcc ttc gac ctg gcc gcg ggc cgc ttc ctc tgc acg gtg			480
Leu Asp Gly Ala Phe Asp Leu Ala Ala Gly Arg Phe Leu Cys Thr Val			
145	150	155	160
ccc ggc gtc tac ttc ctc agc ctc aac gtg cac acc tgg aac tac aag			528
Pro Gly Val Tyr Phe Leu Ser Leu Asn Val His Thr Trp Asn Tyr Lys			
	165	170	175
gag acc tac ctg cac atc atg ctg aac cgg cgg ccc gcg gcc gtg ctc			576
Glu Thr Tyr Leu His Ile Met Leu Asn Arg Arg Pro Ala Ala Val Leu			
	180	185	190
tac gcg cag ccc agc gag cgc agc gtc atg cag gcc cag agc ctg atg			624
Tyr Ala Gln Pro Ser Glu Arg Ser Val Met Gln Ala Gln Ser Leu Met			
	195	200	205
ctg ctg ctg gcg gcg ggc gac gcc gtc tgg gtg cgc atg ttc cag cgc			672
Leu Leu Leu Ala Ala Gly Asp Ala Val Trp Val Arg Met Phe Gln Arg			
	210	215	220
gac cgg gac aac gcc atc tac ggc gag cac gga gac ctc tac atc acc			720
Asp Arg Asp Asn Ala Ile Tyr Gly Glu His Gly Asp Leu Tyr Ile Thr			
225	230	235	240
ttc agc ggc cac ctg gtc aag ccg gcc gcc gag ctg tag			759
Phe Ser Gly His Leu Val Lys Pro Ala Ala Glu Leu *			
	245	250	

<210> 52

<211> 252

<212> PRT

<213> Homo sapiens

<400> 52

Met Ala Ala Pro Ala Leu Leu Leu Leu Ala Leu Leu Leu Pro Val Gly	
1	5
Ala Trp Pro Gly Leu Pro Arg Arg Pro Cys Val His Cys Cys Arg Pro	
	20
Ala Trp Pro Pro Gly Pro Tyr Ala Arg Val Ser Asp Arg Asp Leu Trp	
	35
	40
	45

Arg Gly Asp Leu Trp Arg Gly Leu Pro Arg Val Arg Pro Thr Ile Asp
 50 55 60
 Ile Glu Ile Leu Lys Gly Glu Lys Gly Glu Ala Gly Val Arg Gly Arg
 65 70 75 80
 Ala Gly Arg Ser Gly Lys Glu Gly Pro Pro Gly Ala Arg Gly Leu Gln
 85 90 95
 Gly Arg Arg Gly Gln Lys Gly Gln Val Gly Pro Pro Gly Ala Ala Cys
 100 105 110
 Arg Arg Ala Tyr Ala Ala Phe Ser Val Gly Arg Arg Glu Gly Leu His
 115 120 125
 Ser Ser Asp His Phe Gln Ala Val Pro Phe Asp Thr Glu Leu Val Asn
 130 135 140
 Leu Asp Gly Ala Phe Asp Leu Ala Ala Gly Arg Phe Leu Cys Thr Val
 145 150 155 160
 Pro Gly Val Tyr Phe Leu Ser Leu Asn Val His Thr Trp Asn Tyr Lys
 165 170 175
 Glu Thr Tyr Leu His Ile Met Leu Asn Arg Arg Pro Ala Ala Val Leu
 180 185 190
 Tyr Ala Gln Pro Ser Glu Arg Ser Val Met Gln Ala Gln Ser Leu Met
 195 200 205
 Leu Leu Leu Ala Ala Gly Asp Ala Val Trp Val Arg Met Phe Gln Arg
 210 215 220
 Asp Arg Asp Asn Ala Ile Tyr Gly Glu His Gly Asp Leu Tyr Ile Thr
 225 230 235 240
 Phe Ser Gly His Leu Val Lys Pro Ala Ala Glu Leu
 245 250

<210> 53
 <211> 293
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(293)

<400> 53

atg cag gcc ccc tcg ctc ctc agc gtg gtg gcc gtc tgg ctg acc tgg 48
 Met Gln Ala Pro Ser Leu Leu Ser Val Val Ala Val Trp Leu Thr Trp
 1 5 10 15

gcc aat ggg gcc atc aac cct gtc atc tac gcc atc cgc aat ccc aac 96
 Ala Asn Gly Ala Ile Asn Pro Val Ile Tyr Ala Ile Arg Asn Pro Asn

20					25					30						
att	tcg	atg	ctc	cta	ggg	cgc	aac	cgc	gag	gag	ggc	tac	cgg	act	agg	144
Ile	Ser	Met	Leu	Leu	Gly	Arg	Asn	Arg	Glu	Glu	Gly	Tyr	Arg	Thr	Arg	
		35					40					45				
aat	gtg	gac	gct	ttc	ctg	ccc	agc	cag	ggc	ccg	ggt	ctg	caa	gcc	aga	192
Asn	Val	Asp	Ala	Phe	Leu	Pro	Ser	Gln	Gly	Pro	Gly	Leu	Gln	Ala	Arg	
	50					55				60						
agc	cgc	agt	cgc	ctt	cga	aac	cgc	tat	gcc	aac	cgg	ctg	ggg	gcc	tgc	240
Ser	Arg	Ser	Arg	Leu	Arg	Asn	Arg	Tyr	Ala	Asn	Arg	Leu	Gly	Ala	Cys	
	65				70				75					80		
aac	agg	atg	tcc	tct	tcc	aac	ccg	gcc	agc	gga	gtg	gca	ggg	gac	gtg	288
Asn	Arg	Met	Ser	Ser	Ser	Asn	Pro	Ala	Ser	Gly	Val	Ala	Gly	Asp	Val	
				85				90						95		
gcc	at															293
Ala																

<210> 54
 <211> 97
 <212> PRT
 <213> Homo sapiens

<400> 54

Met	Gln	Ala	Pro	Ser	Leu	Leu	Ser	Val	Val	Ala	Val	Trp	Leu	Thr	Trp	
1				5				10					15			
Ala	Asn	Gly	Ala	Ile	Asn	Pro	Val	Ile	Tyr	Ala	Ile	Arg	Asn	Pro	Asn	
		20					25					30				
Ile	Ser	Met	Leu	Leu	Gly	Arg	Asn	Arg	Glu	Glu	Gly	Tyr	Arg	Thr	Arg	
	35					40					45					
Asn	Val	Asp	Ala	Phe	Leu	Pro	Ser	Gln	Gly	Pro	Gly	Leu	Gln	Ala	Arg	
	50				55					60						
Ser	Arg	Ser	Arg	Leu	Arg	Asn	Arg	Tyr	Ala	Asn	Arg	Leu	Gly	Ala	Cys	
65				70				75				80				
Asn	Arg	Met	Ser	Ser	Ser	Asn	Pro	Ala	Ser	Gly	Val	Ala	Gly	Asp	Val	
				85				90						95		
Ala																

<210> 55
 <211> 258
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(258)

<400> 55

atg	tca	ccg	ccg	ccg	ccg	ctg	ctg	ctg	ctg	ctg	ctg	ctg	ctg	agt	ctg	gcg	48
Met	Ser	Pro	Pro	Pro	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Ser	Leu	Ala	
1				5					10						15		

ctg	ctg	ggc	gcc	cgg	gcc	cgc	gcc	gag	ccc	gcc	ggg	agt	gcc	gtc	ccc	96
Leu	Leu	Gly	Ala	Arg	Ala	Arg	Ala	Glu	Pro	Ala	Gly	Ser	Ala	Val	Pro	
			20					25						30		

gcg	cag	agc	cgc	cca	tgc	gtg	gac	tgc	cac	gcc	ttc	gag	ttc	atg	cag	144
Ala	Gln	Ser	Arg	Pro	Cys	Val	Asp	Cys	His	Ala	Phe	Glu	Phe	Met	Gln	
		35					40					45				

cgc	gcc	ctg	cag	gac	ctg	cgg	aag	aca	gcc	tgc	agc	ctg	gac	gcg	cgg	192
Arg	Ala	Leu	Gln	Asp	Leu	Arg	Lys	Thr	Ala	Cys	Ser	Leu	Asp	Ala	Arg	
		50				55					60					

acg	gag	acc	cta	ctg	ctg	cag	gca	gag	cgc	cgt	gcc	ctg	tgt	gcc	tgc	240
Thr	Glu	Thr	Leu	Leu	Leu	Gln	Ala	Glu	Arg	Arg	Ala	Leu	Cys	Ala	Cys	
65					70				75					80		

tgg	cca	gcg	ggg	cac	tga											258
Trp	Pro	Ala	Gly	His	*											
				85												

<210> 56
 <211> 85
 <212> PRT
 <213> Homo sapiens

<400> 56

Met	Ser	Pro	Pro	Pro	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Ser	Leu	Ala	
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	--

1 5 10 15
 Leu Leu Gly Ala Arg Ala Arg Ala Glu Pro Ala Gly Ser Ala Val Pro
 20 25 30
 Ala Gln Ser Arg Pro Cys Val Asp Cys His Ala Phe Glu Phe Met Gln
 35 40 45
 Arg Ala Leu Gln Asp Leu Arg Lys Thr Ala Cys Ser Leu Asp Ala Arg
 50 55 60
 Thr Glu Thr Leu Leu Leu Gln Ala Glu Arg Arg Ala Leu Cys Ala Cys
 65 70 75 80
 Trp Pro Ala Gly His
 85

<210> 57
 <211> 570
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(570)

<400> 57
 atg gag gaa caa gcc aca cag ggg gtt cca aag tct cca ggg gat gct 48
 Met Glu Glu Gln Ala Thr Gln Gly Val Pro Lys Ser Pro Gly Asp Ala
 1 5 10 15
 gag gaa gcc ttc ctt gcc ctg tcc tgg gtc ttg gcc agc ggt ggg ctc 96
 Glu Glu Ala Phe Leu Ala Leu Ser Trp Val Leu Ala Ser Gly Gly Leu
 20 25 30
 ccc agg gac ctc acc agg acg gca ttt tgc gag agc cga agc cgg aag 144
 Pro Arg Asp Leu Thr Arg Thr Ala Phe Cys Glu Ser Arg Ser Arg Lys
 35 40 45
 cgg cct cgg ggt gcg ctg cac cgc ctc ttc cgg ggc ctc tct agg ccg 192
 Arg Pro Arg Gly Ala Leu His Arg Leu Phe Arg Gly Leu Ser Arg Pro
 50 55 60
 gag cgc ggg att tcg gtg gcc ggg aga ggc cgg aac ggc ttc gcg ggg 240
 Glu Arg Gly Ile Ser Val Ala Gly Arg Gly Arg Asn Gly Phe Ala Gly
 65 70 75 80
 cag cgg cgc ctc ctg gcg ggc ctg ggg tca ggc agt ccg tgg ggg gtc 288

F03290 "CE2E360"

Gln Arg Arg Leu Leu Ala Gly Leu Gly Ser Gly Ser Pro Trp Gly Val
 85 90 95

tgg ctg gct ccc tgc agt aca cac ctg cgc cga tgc cca gcg ttg agg 336
 Trp Leu Ala Pro Cys Ser Thr His Leu Arg Arg Cys Pro Ala Leu Arg
 100 105 110

ccc tac cca tcc cgg ggg acc ttt ccc ctc ccg cct ccc gcc ctt ctg 384
 Pro Tyr Pro Ser Arg Gly Thr Phe Pro Leu Pro Pro Pro Ala Leu Leu
 115 120 125

tcg gct ttc ttc cca cgg atc tgc cag gaa gcc ttc cag gac tgt cct 432
 Ser Ala Phe Phe Pro Arg Ile Cys Gln Glu Ala Phe Gln Asp Cys Pro
 130 135 140

gga gca tca agg ctc gac cgc acg gcc atg ggt acc gac cat ccc agc 480
 Gly Ala Ser Arg Leu Asp Arg Thr Ala Met Gly Thr Asp His Pro Ser
 145 150 155 160

cac acg gct ggg caa cgt gtg gtg ggt cac cgc gca gcc aga ctc cgg 528
 His Thr Ala Gly Gln Arg Val Val Gly His Arg Ala Ala Arg Leu Arg
 165 170 175

ctg gtg acc gcc agg ggt cag cag agg cct cct ttt gca tag 570
 Leu Val Thr Ala Arg Gly Gln Gln Arg Pro Pro Phe Ala *
 180 185

<210> 58
 <211> 189
 <212> PRT
 <213> Homo sapiens

<400> 58
 Met Glu Glu Gln Ala Thr Gln Gly Val Pro Lys Ser Pro Gly Asp Ala
 1 5 10 15
 Glu Glu Ala Phe Leu Ala Leu Ser Trp Val Leu Ala Ser Gly Gly Leu
 20 25 30
 Pro Arg Asp Leu Thr Arg Thr Ala Phe Cys Glu Ser Arg Ser Arg Lys
 35 40 45
 Arg Pro Arg Gly Ala Leu His Arg Leu Phe Arg Gly Leu Ser Arg Pro
 50 55 60
 Glu Arg Gly Ile Ser Val Ala Gly Arg Gly Arg Asn Gly Phe Ala Gly

65 70 75 80
 Gln Arg Arg Leu Leu Ala Gly Leu Gly Ser Gly Ser Pro Trp Gly Val
 85 90 95
 Trp Leu Ala Pro Cys Ser Thr His Leu Arg Arg Cys Pro Ala Leu Arg
 100 105 110
 Pro Tyr Pro Ser Arg Gly Thr Phe Pro Leu Pro Pro Pro Ala Leu Leu
 115 120 125
 Ser Ala Phe Phe Pro Arg Ile Cys Gln Glu Ala Phe Gln Asp Cys Pro
 130 135 140
 Gly Ala Ser Arg Leu Asp Arg Thr Ala Met Gly Thr Asp His Pro Ser
 145 150 155 160
 His Thr Ala Gly Gln Arg Val Val Gly His Arg Ala Ala Arg Leu Arg
 165 170 175
 Leu Val Thr Ala Arg Gly Gln Gln Arg Pro Pro Phe Ala
 180 185

<210> 59
 <211> 498
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(498)

<400> 59

atg aga aag ata ctt ttc cta aac ctg tgg atc tca cta gtg aaa gca 48
 Met Arg Lys Ile Leu Phe Leu Asn Leu Trp Ile Ser Leu Val Lys Ala
 1 5 10 15

agc aca tac cag gga gaa cag gaa gcc aga ggc acc aac aac act gag 96
 Ser Thr Tyr Gln Gly Glu Gln Glu Ala Arg Gly Thr Asn Asn Thr Glu
 20 25 30

ttt gat gca aaa aag ggg gac ttt agt tca ggc tgc ata aaa aca gga 144
 Phe Asp Ala Lys Lys Gly Asp Phe Ser Ser Gly Cys Ile Lys Thr Gly
 35 40 45

ggc cga ttc aat gca tgg ata aac ggg tct gtc tac ctc cat cgc cgc 192
 Gly Arg Phe Asn Ala Trp Ile Asn Gly Ser Val Tyr Leu His Arg Arg
 50 55 60

tcg tca agt gca atg gga acc gat gaa aca ctg aag gcc tct ggg ctg 240

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<210> 60
<211> 165
<212> PRT
<213> Homo sapiens
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<400> 60															
Met	Arg	Lys	Ile	Leu	Phe	Leu	Asn	Leu	Trp	Ile	Ser	Leu	Val	Lys	Ala
1				5					10					15	
Ser	Thr	Tyr	Gln	Gly	Glu	Gln	Glu	Ala	Arg	Gly	Thr	Asn	Asn	Thr	Glu
			20					25					30		
Phe	Asp	Ala	Lys	Lys	Gly	Asp	Phe	Ser	Ser	Gly	Cys	Ile	Lys	Thr	Gly
		35					40					45			
Gly	Arg	Phe	Asn	Ala	Trp	Ile	Asn	Gly	Ser	Val	Tyr	Leu	His	Arg	Arg
	50					55					60				
Ser	Ser	Ser	Ala	Met	Gly	Thr	Asp	Glu	Thr	Leu	Lys	Ala	Ser	Gly	Leu


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<210> 61
<211> 462
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> (1)...(462)
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atg cac ctg cgg ctg cta cca cta ctg ctt ctg cta atg ctg tcg tta 48
Met His Leu Arg Leu Leu Pro Leu Leu Leu Leu Leu Met Leu Ser Leu
1 5 10 15

aaa ctg atg gct acc acg cgt ggt cga tta tgt gct acg tct tgt gca 96
Lys Leu Met Ala Thr Thr Arg Gly Arg Leu Cys Ala Thr Ser Cys Ala
20 25 30

aga ctc caa gtt ctt cag tgt cga act ctt gga ctt aca cca gtg gtt 144
Arg Leu Gln Val Leu Gln Cys Arg Thr Leu Gly Leu Thr Pro Val Val
35 40 45

tgc cag cgg ctc tcg agc ctt ctg cta cag act gaa ggc tac gct ctc 192
Cys Gln Arg Leu Ser Ser Leu Leu Leu Gln Thr Glu Gly Tyr Ala Leu
50 55 60

ggc ttc cct act ttt agg gct ttg gga ctt gaa ctg gct tcc ttg ctc 240
Gly Phe Pro Thr Phe Arg Ala Leu Gly Leu Glu Leu Ala Ser Leu Leu
65 70 75 80

<400> 62																
Met	His	Leu	Arg	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	Met	Leu	Ser	Leu	
1				5					10					15		
Lys	Leu	Met	Ala	Thr	Thr	Arg	Gly	Arg	Leu	Cys	Ala	Thr	Ser	Cys	Ala	
			20					25					30			
Arg	Leu	Gln	Val	Leu	Gln	Cys	Arg	Thr	Leu	Gly	Leu	Thr	Pro	Val	Val	
		35					40					45				
Cys	Gln	Arg	Leu	Ser	Ser	Leu	Leu	Leu	Gln	Thr	Glu	Gly	Tyr	Ala	Leu	
	50					55					60					
Gly	Phe	Pro	Thr	Phe	Arg	Ala	Leu	Gly	Leu	Glu	Leu	Ala	Ser	Leu	Leu	
65					70					75					80	
Leu	Ser	Leu	Gln	Met	Ala	Tyr	Cys	Gly	Thr	Leu	Pro	Cys	Asp	His	Asn	
				85					90					95		
Ala	Thr	Leu	Ser	Pro	Ala	Gly	Lys	Pro	Glu	Gln	Ile	Lys	Met	Ala	Ser	
			100					105					110			
Ala	Pro	Gly	Gly	Asn	Gly	Asn	Phe	Gln	Arg	Asp	Arg	Lys	Lys	Met	Ile	

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<210> 63
<211> 315
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(315)
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<400> 63																
atg	aag	gtt	gga	gga	ctc	agc	aag	aca	gct	ttt	tct	tct	acc	ttc	ttc	48
Met	Lys	Val	Gly	Gly	Leu	Ser	Lys	Thr	Ala	Phe	Ser	Ser	Thr	Phe	Phe	
1				5				10						15		
tcc	ctg	ctt	ttt	cca	gcc	tca	ctg	gca	gct	gat	tgg	atg	gtg	ccc	acc	96
Ser	Leu	Leu	Phe	Pro	Ala	Ser	Leu	Ala	Ala	Asp	Trp	Met	Val	Pro	Thr	
			20				25						30			
aca	ttg	tgg	aca	tta	gaa	cta	aag	ttt	ctt	ggg	cct	tta	gac	ttg	agg	144
Thr	Leu	Trp	Thr	Leu	Glu	Leu	Lys	Phe	Leu	Gly	Pro	Leu	Asp	Leu	Arg	
			35				40						45			
gct	tac	atc	agt	ggc	ccc	caa	ttt	ctc	aaa	ctt	tca	act	tca	aat	aaa	192
Ala	Tyr	Ile	Ser	Gly	Pro	Gln	Phe	Leu	Lys	Leu	Ser	Thr	Ser	Asn	Lys	
50						55						60				
gtt	aca	tcc	tca	gat	ccc	cca	ggt	tct	tct	ttg	gac	tca	gac	tgg	att	240
Val	Thr	Ser	Ser	Asp	Pro	Pro	Gly	Ser	Ser	Leu	Asp	Ser	Asp	Trp	Ile	
65				70						75				80		
aca	tca	aaa	gct	ttc	ctg	gtt	ctt	cag	ttt	gaa	gac	agc	atg	ttg	tgg	288
Thr	Ser	Lys	Ala	Phe	Leu	Val	Leu	Gln	Phe	Glu	Asp	Ser	Met	Leu	Trp	
				85				90						95		
gac	ttc	tca	acc	tct	ata	att	gtg	tga								315
Asp	Phe	Ser	Thr	Ser	Ile	Ile	Val	*								
			100													

<210> 64
 <211> 104
 <212> PRT
 <213> Homo sapiens

<400> 64
 Met Lys Val Gly Gly Leu Ser Lys Thr Ala Phe Ser Ser Thr Phe Phe
 1 5 10 15
 Ser Leu Leu Phe Pro Ala Ser Leu Ala Ala Asp Trp Met Val Pro Thr
 20 25 30
 Thr Leu Trp Thr Leu Glu Leu Lys Phe Leu Gly Pro Leu Asp Leu Arg
 35 40 45
 Ala Tyr Ile Ser Gly Pro Gln Phe Leu Lys Leu Ser Thr Ser Asn Lys
 50 55 60
 Val Thr Ser Ser Asp Pro Pro Gly Ser Ser Leu Asp Ser Asp Trp Ile
 65 70 75 80
 Thr Ser Lys Ala Phe Leu Val Leu Gln Phe Glu Asp Ser Met Leu Trp
 85 90 95
 Asp Phe Ser Thr Ser Ile Ile Val
 100

<210> 65
 <211> 339
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(339)

<400> 65
 atg tgg gat gaa tca agt aca acc aca tgt gtt cca aag gtc aat gag 48
 Met Trp Asp Glu Ser Ser Thr Thr Thr Cys Val Pro Lys Val Asn Glu
 1 5 10 15
 agg ctc ttc gtg ctt tta gca tta att ttg cct cca ttg aca tca gag 96
 Arg Leu Phe Val Leu Leu Ala Leu Ile Leu Pro Pro Leu Thr Ser Glu
 20 25 30
 att ctg gat aac aac cgc ctc aga caa ata ttt gta gtg ttt ggc cct 144
 Ile Leu Asp Asn Asn Arg Leu Arg Gln Ile Phe Val Val Phe Gly Pro

<210> 67
 <211> 264
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(264)

<400> 67

atg gct gtc tta gta ctt cgc ctg aca gtt gtc ctg gga ctg ctt gtc	48
Met Ala Val Leu Val Leu Arg Leu Thr Val Val Leu Gly Leu Leu Val	
1 5 10 15	

tta ttc ctg acc tgc tat gca gac gac aaa cca gac aag cca gac gac	96
Leu Phe Leu Thr Cys Tyr Ala Asp Asp Lys Pro Asp Lys Pro Asp Asp	
20 25 30	

aag cca gac gac tcg ggc aaa gac cca aag cca gac ttc ccc aaa ttc	144
Lys Pro Asp Asp Ser Gly Lys Asp Pro Lys Pro Asp Phe Pro Lys Phe	
35 40 45	

cta agc ctc ctg ggc aca gag atc att gag aat gca gtc gag ttc atc	192
Leu Ser Leu Leu Gly Thr Glu Ile Ile Glu Asn Ala Val Glu Phe Ile	
50 55 60	

ctc cgc tcc atg tcc agg agc aca gga ttt atg gaa ttt gat gat aat	240
Leu Arg Ser Met Ser Arg Ser Thr Gly Phe Met Glu Phe Asp Asp Asn	
65 70 75 80	

gaa gga aaa cat tca tca aag tga	264
Glu Gly Lys His Ser Ser Lys *	
85	

<210> 68
 <211> 87
 <212> PRT
 <213> Homo sapiens

<400> 68

Met Ala Val Leu Val Leu Arg Leu Thr Val Val Leu Gly Leu Leu Val

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<210> 69
<211> 357
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (1)...(357)

<400> 69																
atg	ggc	tca	aag	aag	gta	gaa	ggg	ttg	ggt	ccg	gac	gaa	ctg	ctg	ctg	48
Met	Gly	Ser	Lys	Lys	Val	Glu	Gly	Leu	Gly	Pro	Asp	Glu	Leu	Leu	Leu	
1			5			10			15							
tta	ctg	ttg	ctg	ctg	ctg	ctg	ctg	ctg	ctg	ctg	ctg	ctg	ctg	ctg	ctg	96
Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	
20			25			30										
tcc	agc	agg	gca	gaa	gac	tgc	agt	ggc	cgg	gtg	tcc	agt	gtt	gtt	ggg	144
Ser	Ser	Arg	Ala	Glu	Asp	Cys	Ser	Gly	Arg	Val	Ser	Ser	Val	Val	Gly	
35			40			45										
ccc	agt	ggg	agt	gaa	ctg	agc	tca	cca	ctg	tcc	ttg	cta	tca	gtc	cca	192
Pro	Ser	Gly	Ser	Glu	Leu	Ser	Ser	Pro	Leu	Ser	Leu	Leu	Ser	Val	Pro	
50			55			60										
ggg	ccg	cca	ctc	act	aca	atg	ata	gcc	ccc	aaa	ccc	agt	cat	aca	aga	240
Gly	Pro	Pro	Leu	Thr	Thr	Met	Ile	Ala	Pro	Lys	Pro	Ser	His	Thr	Arg	
65			70			75			80							
gga	agt	aac	ctg	aaa	tta	gtc	acc	aca	gga	gac	agg	gac	aca	aga	cct	288

Gly Ser Asn Leu Lys Leu Val Thr Thr Gly Asp Arg Asp Thr Arg Pro
 85 90 95

aca gaa gaa gac tcg tgg tca aca tgt ctg ctg tgg cca tac ttc aag 336
 Thr Glu Glu Asp Ser Trp Ser Thr Cys Leu Leu Trp Pro Tyr Phe Lys
 100 105 110

acg ggc tac cag ggc aat tga 357
 Thr Gly Tyr Gln Gly Asn *
 115

<210> 70
 <211> 118
 <212> PRT
 <213> Homo sapiens

<400> 70
 Met Gly Ser Lys Lys Val Glu Gly Leu Gly Pro Asp Glu Leu Leu Leu
 1 5 10 15
 Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu
 20 25 30
 Ser Ser Arg Ala Glu Asp Cys Ser Gly Arg Val Ser Ser Val Val Gly
 35 40 45
 Pro Ser Gly Ser Glu Leu Ser Ser Pro Leu Ser Leu Leu Ser Val Pro
 50 55 60
 Gly Pro Pro Leu Thr Thr Met Ile Ala Pro Lys Pro Ser His Thr Arg
 65 70 75 80
 Gly Ser Asn Leu Lys Leu Val Thr Thr Gly Asp Arg Asp Thr Arg Pro
 85 90 95
 Thr Glu Glu Asp Ser Trp Ser Thr Cys Leu Leu Trp Pro Tyr Phe Lys
 100 105 110
 Thr Gly Tyr Gln Gly Asn
 115

<210> 71
 <211> 474
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(474)

<400> 71

atg aag gca gcc tgc tct tcc ctc tgc ttg tca ctg ttg gct tta gaa	48
Met Lys Ala Ala Cys Ser Ser Leu Cys Leu Ser Leu Leu Ala Leu Glu	
1 5 10 15	
gcc acc tgg gga tta gga gca gca ggt gac aag cac ttt gaa gat gcc	96
Ala Thr Trp Gly Leu Gly Ala Ala Gly Asp Lys His Phe Glu Asp Ala	
20 25 30	
ctc cca gtg tcg ggg ctg gct cct gat gtg cag tgt cgg cac ctc ggc	144
Leu Pro Val Ser Gly Leu Ala Pro Asp Val Gln Cys Arg His Leu Gly	
35 40 45	
act tgg ggc gac tgt tgt ggc tgt gct gat ttg ctc atg atg cgc cac	192
Thr Trp Gly Asp Cys Cys Gly Cys Ala Asp Leu Leu Met Met Arg His	
50 55 60	
gac ctg gac tcc agt tac ttg cac gtg gga tcc cct gct gtc gtc cgc	240
Asp Leu Asp Ser Ser Tyr Leu His Val Gly Ser Pro Ala Val Val Arg	
65 70 75 80	
aag tca ccg agg ggg tgt gga gga gcc ttg cct gac agc cgg agg gag	288
Lys Ser Pro Arg Gly Cys Gly Gly Ala Leu Pro Asp Ser Arg Arg Glu	
85 90 95	
ctg gag tct gaa atg tca gct gct ctt ttt aca gaa cgt tat gtc aca	336
Leu Glu Ser Glu Met Ser Ala Ala Leu Phe Thr Glu Arg Tyr Val Thr	
100 105 110	
ggc ctt caa ata aga gcg ccc aat ttc ggc tca aga cgc gca ctg agc	384
Gly Leu Gln Ile Arg Ala Pro Asn Phe Gly Ser Arg Arg Ala Leu Ser	
115 120 125	
aga gat atg gag ctg gcc ctg acc acg ctg tgg agc ccg tgc tgg tcc	432
Arg Asp Met Glu Leu Ala Leu Thr Thr Leu Trp Ser Pro Cys Trp Ser	
130 135 140	
ctc aag cct cca gcc acc tgc acg cgg ggc cag cca ggc cag	474
Leu Lys Pro Pro Ala Thr Cys Thr Arg Gly Gln Pro Gly Gln	
145 150 155	

<210> 72
 <211> 158
 <212> PRT
 <213> Homo sapiens

<400> 72

Met Lys Ala Ala Cys Ser Ser Leu Cys Leu Ser Leu Leu Ala Leu Glu
 1 5 10 15
 Ala Thr Trp Gly Leu Gly Ala Ala Gly Asp Lys His Phe Glu Asp Ala
 20 25 30
 Leu Pro Val Ser Gly Leu Ala Pro Asp Val Gln Cys Arg His Leu Gly
 35 40 45
 Thr Trp Gly Asp Cys Cys Gly Cys Ala Asp Leu Leu Met Met Arg His
 50 55 60
 Asp Leu Asp Ser Ser Tyr Leu His Val Gly Ser Pro Ala Val Val Arg
 65 70 75 80
 Lys Ser Pro Arg Gly Cys Gly Gly Ala Leu Pro Asp Ser Arg Arg Glu
 85 90 95
 Leu Glu Ser Glu Met Ser Ala Ala Leu Phe Thr Glu Arg Tyr Val Thr
 100 105 110
 Gly Leu Gln Ile Arg Ala Pro Asn Phe Gly Ser Arg Arg Ala Leu Ser
 115 120 125
 Arg Asp Met Glu Leu Ala Leu Thr Thr Leu Trp Ser Pro Cys Trp Ser
 130 135 140
 Leu Lys Pro Pro Ala Thr Cys Thr Arg Gly Gln Pro Gly Gln
 145 150 155

<210> 73
 <211> 411
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> (1)...(411)

<400> 73

atg cgc ccg ctg ctg ctg acc aag agg gca tta ctt ctt cca tcc tca 48
 Met Arg Pro Leu Leu Leu Thr Lys Arg Ala Leu Leu Leu Pro Ser Ser
 1 5 10 15

cat ctg gct caa gcg gaa atg aag ctg gcc ttc ccc atg ttc aaa gtc 96
 His Leu Ala Gln Ala Glu Met Lys Leu Ala Phe Pro Met Phe Lys Val

	20	25	30	
cag gca tgc cag ccc gat tca cac tcg gct cag aga cct ctg acc caa				144
Gln Ala Cys Gln Pro Asp Ser His Ser Ala Gln Arg Pro Leu Thr Gln				
	35	40	45	
tta ccc ctg gtt cct ggt gag cct cgc tgc aag acg gaa gcc tgt cac				192
Leu Pro Leu Val Pro Gly Glu Pro Arg Cys Lys Thr Glu Ala Cys His				
	50	55	60	
ccc ggc ccc atc cct caa ggt gaa acg tgc tgg gcc ctg ctc ctc cac				240
Pro Gly Pro Ile Pro Gln Gly Glu Thr Cys Trp Ala Leu Leu Leu His				
	65	70	75	80
tgc tct gat cat caa gcc ttc atc cag ctc tgt gct ggg gcc acg gac				288
Cys Ser Asp His Gln Ala Phe Ile Gln Leu Cys Ala Gly Ala Thr Asp				
	85	90	95	
agc gtg tct gga ggc acc att gac gtg gga cag cat cat ggg acc gca				336
Ser Val Ser Gly Gly Thr Ile Asp Val Gly Gln His His Gly Thr Ala				
	100	105	110	
cat gca aga cat gcc cca aaa tgg tct cag aac cac act gct tct ggt				384
His Ala Arg His Ala Pro Lys Trp Ser Gln Asn His Thr Ala Ser Gly				
	115	120	125	
gca gcc cac agc ggt ctt ttc cta taa				411
Ala Ala His Ser Gly Leu Phe Leu *				
	130	135		

<210> 74

<211> 136

<212> PRT

<213> Homo sapiens

<400> 74

Met Arg Pro Leu Leu Thr Lys Arg Ala Leu Leu Leu Pro Ser Ser				
1	5	10	15	
His Leu Ala Gln Ala Glu Met Lys Leu Ala Phe Pro Met Phe Lys Val				
	20	25	30	
Gln Ala Cys Gln Pro Asp Ser His Ser Ala Gln Arg Pro Leu Thr Gln				
	35	40	45	

Leu Pro Leu Val Pro Gly Glu Pro Arg Cys Lys Thr Glu Ala Cys His
 50 55 60
 Pro Gly Pro Ile Pro Gln Gly Glu Thr Cys Trp Ala Leu Leu Leu His
 65 70 75 80
 Cys Ser Asp His Gln Ala Phe Ile Gln Leu Cys Ala Gly Ala Thr Asp
 85 90 95
 Ser Val Ser Gly Gly Thr Ile Asp Val Gly Gln His His Gly Thr Ala
 100 105 110
 His Ala Arg His Ala Pro Lys Trp Ser Gln Asn His Thr Ala Ser Gly
 115 120 125
 Ala Ala His Ser Gly Leu Phe Leu
 130 135

<210> 75

<211> 678

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(678)

<400> 75

atg tac ttg gtg gcg ggg gac agg ggg ttg gcc ggc tgc ggg cac ctc	48
Met Tyr Leu Val Ala Gly Asp Arg Gly Leu Ala Gly Cys Gly His Leu	
1 5 10 15	
ctg gtc tcg ctg ctg ggg ctg ctg ctg ctg ctg gcg cgc tcc ggc acc	96
Leu Val Ser Leu Leu Gly Leu Leu Leu Leu Leu Ala Arg Ser Gly Thr	
20 25 30	
cgg gcg ctg gtc tgc ctg ccc tgt gac gag tcc aag tgc gag gag ccc	144
Arg Ala Leu Val Cys Leu Pro Cys Asp Glu Ser Lys Cys Glu Glu Pro	
35 40 45	
agg aac tgc ccg ggg agc atc gtg cag ggc gtc tgc ggc tgc tgc tac	192
Arg Asn Cys Pro Gly Ser Ile Val Gln Gly Val Cys Gly Cys Cys Tyr	
50 55 60	
acg tgc gcc agc cag agg aac gag agc tgc ggc ggc acc ttc ggg att	240
Thr Cys Ala Ser Gln Arg Asn Glu Ser Cys Gly Gly Thr Phe Gly Ile	
65 70 75 80	

F002390" 1222000

tac gga acc tgc gac cgg ggg ctg cgt tgt gtc atc cgc ccc ccg ctc	288
Tyr Gly Thr Cys Asp Arg Gly Leu Arg Cys Val Ile Arg Pro Pro Leu	
85 90 95	
aat ggc gac tcc ctc acc gag tac gaa gcg ggc gtt tgc gaa ggt acg	336
Asn Gly Asp Ser Leu Thr Glu Tyr Glu Ala Gly Val Cys Glu Gly Thr	
100 105 110	
gcc gcc cgc tgc ggg ccc cct ccc acc tgg cct gcg ccg ccc cct cgg	384
Ala Ala Arg Cys Gly Pro Pro Pro Thr Trp Pro Ala Pro Pro Pro Arg	
115 120 125	
cgc tgg ttg tgc cga aca aag ttt ggg cga gac ttt ctg gag gaa aga	432
Arg Trp Leu Cys Arg Thr Lys Phe Gly Arg Asp Phe Leu Glu Glu Arg	
130 135 140	
ggg ctc tgc ggg aag agg ggc ggc cgc cgc ccc cag gag agt gcc ccc	480
Gly Leu Cys Gly Lys Arg Gly Gly Arg Arg Pro Gln Glu Ser Ala Pro	
145 150 155 160	
gcg gcc ctg cgt tcc ctc tcc ttg ttc ccc ccg acg ctt agg cag tcg	528
Ala Ala Leu Arg Ser Leu Ser Leu Phe Pro Pro Thr Leu Arg Gln Ser	
165 170 175	
cgg gcg agg ttg ggt atg gct gcc tgc ctc cag gaa aat cac cta gaa	576
Arg Ala Arg Leu Gly Met Ala Ala Cys Leu Gln Glu Asn His Leu Glu	
180 185 190	
gcc aga gaa aca agt gtg gat cct gaa ccc ctg aga aag aaa tct gga	624
Ala Arg Glu Thr Ser Val Asp Pro Glu Pro Leu Arg Lys Lys Ser Gly	
195 200 205	
tgg aag aca tct ttg gag gat cga agg cag agt tta gaa aaa tta atg	672
Trp Lys Thr Ser Leu Glu Asp Arg Arg Gln Ser Leu Glu Lys Leu Met	
210 215 220	
aag tga	678
Lys *	
225	

<210> 76

<211> 225

<212> PRT

<213> Homo sapiens

<400> 76

Met Tyr Leu Val Ala Gly Asp Arg Gly Leu Ala Gly Cys Gly His Leu
 1 5 10 15
 Leu Val Ser Leu Leu Gly Leu Leu Leu Leu Ala Arg Ser Gly Thr
 20 25 30
 Arg Ala Leu Val Cys Leu Pro Cys Asp Glu Ser Lys Cys Glu Glu Pro
 35 40 45
 Arg Asn Cys Pro Gly Ser Ile Val Gln Gly Val Cys Gly Cys Cys Tyr
 50 55 60
 Thr Cys Ala Ser Gln Arg Asn Glu Ser Cys Gly Gly Thr Phe Gly Ile
 65 70 75 80
 Tyr Gly Thr Cys Asp Arg Gly Leu Arg Cys Val Ile Arg Pro Pro Leu
 85 90 95
 Asn Gly Asp Ser Leu Thr Glu Tyr Glu Ala Gly Val Cys Glu Gly Thr
 100 105 110
 Ala Ala Arg Cys Gly Pro Pro Pro Thr Trp Pro Ala Pro Pro Pro Arg
 115 120 125
 Arg Trp Leu Cys Arg Thr Lys Phe Gly Arg Asp Phe Leu Glu Glu Arg
 130 135 140
 Gly Leu Cys Gly Lys Arg Gly Gly Arg Arg Pro Gln Glu Ser Ala Pro
 145 150 155 160
 Ala Ala Leu Arg Ser Leu Ser Leu Phe Pro Pro Thr Leu Arg Gln Ser
 165 170 175
 Arg Ala Arg Leu Gly Met Ala Ala Cys Leu Gln Glu Asn His Leu Glu
 180 185 190
 Ala Arg Glu Thr Ser Val Asp Pro Glu Pro Leu Arg Lys Lys Ser Gly
 195 200 205
 Trp Lys Thr Ser Leu Glu Asp Arg Arg Gln Ser Leu Glu Lys Leu Met
 210 215 220
 Lys
 225

<210> 77

<211> 558

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(558)

F00239.222660

<400> 77

atg	gcc	cgg	gcc	agg	gcc	ggg	gcg	ctg	ctg	gcg	ctt	tgg	gtg	ctc	ggg	48
Met	Ala	Arg	Ala	Arg	Ala	Gly	Ala	Leu	Leu	Ala	Leu	Trp	Val	Leu	Gly	
1				5				10						15		

gcc	gcc	gcg	cat	ccg	cag	tgc	ctg	gac	ttc	agg	ccg	ccc	ttc	cgg	ccg	96
Ala	Ala	Ala	His	Pro	Gln	Cys	Leu	Asp	Phe	Arg	Pro	Pro	Phe	Arg	Pro	
			20				25						30			

acg	cag	ccg	ctg	cgc	ctc	tgc	gcg	cag	tac	tgc	gac	ttc	ggc	tgc	tgc	144
Thr	Gln	Pro	Leu	Arg	Leu	Cys	Ala	Gln	Tyr	Ser	Asp	Phe	Gly	Cys	Cys	
		35					40					45				

gat	gag	ggg	cgc	gac	gcc	gag	ctg	acc	cgc	cgc	ttc	tgg	gcc	ctg	gcg	192
Asp	Glu	Gly	Arg	Asp	Ala	Glu	Leu	Thr	Arg	Arg	Phe	Trp	Ala	Leu	Ala	
	50					55					60					

agc	cgc	gtg	gac	gcc	gcc	gag	tgg	gcc	gcg	tgc	gcc	ggc	tac	gcg	agg	240
Ser	Arg	Val	Asp	Ala	Ala	Glu	Trp	Ala	Ala	Cys	Ala	Gly	Tyr	Ala	Arg	
	65				70					75					80	

gac	ctg	ctg	tgc	cag	tcc	gtg	gag	tgg	aca	gac	atg	caa	aga	gat	aat	288
Asp	Leu	Leu	Cys	Gln	Ser	Val	Glu	Trp	Thr	Asp	Met	Gln	Arg	Asp	Asn	
				85				90						95		

gaa	gtc	cta	gcc	aag	ctg	act	ggc	tgg	agc	gcc	cct	ggc	gac	gga	gca	336
Glu	Val	Leu	Ala	Lys	Leu	Thr	Gly	Trp	Ser	Ala	Pro	Gly	Asp	Gly	Ala	
			100					105					110			

gtg	act	gct	gta	gag	aac	tca	ccc	tgt	aag	cta	caa	gat	tca	atg	gat	384
Val	Thr	Ala	Val	Glu	Asn	Ser	Pro	Cys	Lys	Leu	Gln	Asp	Ser	Met	Asp	
		115					120					125				

tct	gga	ttg	ggc	ttt	ggt	gaa	cgg	agg	gct	ctc	gtt	gcc	ttc	cag	atg	432
Ser	Gly	Leu	Gly	Phe	Gly	Glu	Arg	Arg	Ala	Leu	Val	Ala	Phe	Gln	Met	
	130					135					140					

tct	gtt	ctg	ccc	ctc	act	gcg	tct	ctg	gaa	cca	aga	tgg	tgc	ctg	gta	480
Ser	Val	Leu	Pro	Leu	Thr	Ala	Ser	Leu	Glu	Pro	Arg	Trp	Cys	Leu	Val	
	145				150				155					160		

caa	tct	ctg	ctc	agt	aaa	ttc	ttg	gtg	aat	gaa	atg	ttg	ctg	act	aat	528
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<220>

<221> CDS

<222> (1)...(645)

<400> 79

atg	ccc	gcg	gcc	cgg	ccg	ccc	gcc	gcg	gga	ctc	cgc	ggg	atc	tcg	ctg	48
Met	Pro	Ala	Ala	Arg	Pro	Pro	Ala	Ala	Gly	Leu	Arg	Gly	Ile	Ser	Leu	
1				5					10					15		
ttc	ctc	gct	ctg	ctc	ctg	ggg	agc	ccg	gcg	gca	gcg	ctg	gag	cga	ggg	96
Phe	Leu	Ala	Leu	Leu	Leu	Gly	Ser	Pro	Ala	Ala	Ala	Leu	Glu	Arg	Gly	
			20					25					30			
gtg	gtc	agt	gaa	ggc	ttc	ctg	gag	cac	gta	gca	ttt	gaa	ctg	gcc	ctg	144
Val	Val	Ser	Glu	Gly	Phe	Leu	Glu	His	Val	Ala	Phe	Glu	Leu	Ala	Leu	
		35					40					45				
aag	ggg	ata	gga	cag	aca	cag	acc	ctg	gag	tcc	aag	aga	tat	ggg	ttc	192
Lys	Gly	Ile	Gly	Gln	Thr	Gln	Thr	Leu	Glu	Ser	Lys	Arg	Tyr	Gly	Phe	
	50					55					60					
aaa	cct	aat	gct	gtg	atc	ttg	aac	aag	tca	ctt	aac	tct	gag	atg	atg	240
Lys	Pro	Asn	Ala	Val	Ile	Leu	Asn	Lys	Ser	Leu	Asn	Ser	Glu	Met	Met	
	65				70				75					80		
gga	gtg	ggt	ggt	agt	gat	gag	gat	gaa	gag	ggg	aat	tat	gag	ttg	ctg	288
Gly	Val	Gly	Gly	Ser	Asp	Glu	Asp	Glu	Glu	Gly	Asn	Tyr	Glu	Leu	Leu	
				85				90						95		
ttg	tta	ctg	atg	gac	cga	gct	gat	tct	cag	aca	ttt	aaa	agt	gat	cca	336
Leu	Leu	Leu	Met	Asp	Arg	Ala	Asp	Ser	Gln	Thr	Phe	Lys	Ser	Asp	Pro	
			100					105					110			
ggc	att	gaa	aat	cag	gtt	gga	gtg	gaa	aat	gaa	gag	aag	cct	caa	ggt	384
Gly	Ile	Glu	Asn	Gln	Val	Gly	Val	Glu	Asn	Glu	Glu	Lys	Pro	Gln	Gly	
		115				120						125				
ggg	gtc	cca	gga	gct	ctc	ccc	ttt	tcc	cat	gag	aga	ttc	atc	tgg	aat	432
Gly	Val	Pro	Gly	Ala	Leu	Pro	Phe	Ser	His	Glu	Arg	Phe	Ile	Trp	Asn	
	130					135					140					
gat	gac	agt	gga	ttt	aag	agc	aat	aag	gga	ggg	gaa	cgg	ctg	agc	cag	480

Asp Asp Ser Gly Phe Lys Ser Asn Lys Gly Gly Glu Arg Leu Ser Gln
 145 150 155 160

 gga cct gtg gac act cag gat tca act ctg ggc ttg gcc aga gat aag 528
 Gly Pro Val Asp Thr Gln Asp Ser Thr Leu Gly Leu Ala Arg Asp Lys
 165 170 175

 tcc tta gag ttt ggg gca ttt gaa caa ctg aca aga agc cag cat ggc 576
 Ser Leu Glu Phe Gly Ala Phe Glu Gln Leu Thr Arg Ser Gln His Gly
 180 185 190

 cag aat atc ctg aac aga gaa gga agt ggg caa atg aag tta aga gaa 624
 Gln Asn Ile Leu Asn Arg Glu Gly Ser Gly Gln Met Lys Leu Arg Glu
 195 200 205

 agt att aaa gaa aag caa tga 645
 Ser Ile Lys Glu Lys Gln *
 210

<210> 80
 <211> 214
 <212> PRT
 <213> Homo sapiens

<400> 80
 Met Pro Ala Ala Arg Pro Pro Ala Ala Gly Leu Arg Gly Ile Ser Leu
 1 5 10 15
 Phe Leu Ala Leu Leu Leu Gly Ser Pro Ala Ala Ala Leu Glu Arg Gly
 20 25 30
 Val Val Ser Glu Gly Phe Leu Glu His Val Ala Phe Glu Leu Ala Leu
 35 40 45
 Lys Gly Ile Gly Gln Thr Gln Thr Leu Glu Ser Lys Arg Tyr Gly Phe
 50 55 60
 Lys Pro Asn Ala Val Ile Leu Asn Lys Ser Leu Asn Ser Glu Met Met
 65 70 75 80
 Gly Val Gly Gly Ser Asp Glu Asp Glu Glu Gly Asn Tyr Glu Leu Leu
 85 90 95
 Leu Leu Leu Met Asp Arg Ala Asp Ser Gln Thr Phe Lys Ser Asp Pro
 100 105 110
 Gly Ile Glu Asn Gln Val Gly Val Glu Asn Glu Glu Lys Pro Gln Gly
 115 120 125
 Gly Val Pro Gly Ala Leu Pro Phe Ser His Glu Arg Phe Ile Trp Asn

130 135 140
 Asp Asp Ser Gly Phe Lys Ser Asn Lys Gly Gly Glu Arg Leu Ser Gln
 145 150 155 160
 Gly Pro Val Asp Thr Gln Asp Ser Thr Leu Gly Leu Ala Arg Asp Lys
 165 170 175
 Ser Leu Glu Phe Gly Ala Phe Glu Gln Leu Thr Arg Ser Gln His Gly
 180 185 190
 Gln Asn Ile Leu Asn Arg Glu Gly Ser Gly Gln Met Lys Leu Arg Glu
 195 200 205
 Ser Ile Lys Glu Lys Gln
 210

<210> 81
 <211> 303
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(303)

<400> 81
 atg gca gcc ttg ctg ctc ttg acc ctc agc ctg att cag gtc tca ggg 48
 Met Ala Ala Leu Leu Leu Leu Thr Leu Ser Leu Ile Gln Val Ser Gly
 1 5 10 15
 gtg ctg ctg acc tcc agt gtg gac agt ccc tct acc ctg ccg ctg tct 96
 Val Leu Leu Thr Ser Ser Val Asp Ser Pro Ser Thr Leu Pro Leu Ser
 20 25 30
 gca cag aga acc gtc cac cgt ggc ctc ttt aca ttc caa gct gga ttt 144
 Ala Gln Arg Thr Val His Arg Gly Leu Phe Thr Phe Gln Ala Gly Phe
 35 40 45
 tct cct gat cgc tcc agt tct cga ggc aaa aag caa aga gtc tcg ggc 192
 Ser Pro Asp Arg Ser Ser Ser Arg Gly Lys Lys Gln Arg Val Ser Gly
 50 55 60
 tgc aat gac atg gtt tgc ttc ggg ttc tcc ggc gcc gcc tgc ctc ctc 240
 Cys Asn Asp Met Val Cys Phe Gly Phe Ser Gly Ala Ala Cys Leu Leu
 65 70 75 80
 tgt cag atg ccg gtg ttc ggg ggc ggc ttc gtt ggc ttc ctt cct tct 288

Cys Gln Met Pro Val Phe Gly Gly Gly Phe Val Gly Phe Leu Pro Ser
 85 90 95

ctg ttc cag acc taa
 Leu Phe Gln Thr *
 100

303

<210> 82
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 82
 Met Ala Ala Leu Leu Leu Thr Leu Ser Leu Ile Gln Val Ser Gly
 1 5 10 15
 Val Leu Leu Thr Ser Ser Val Asp Ser Pro Ser Thr Leu Pro Leu Ser
 20 25 30
 Ala Gln Arg Thr Val His Arg Gly Leu Phe Thr Phe Gln Ala Gly Phe
 35 40 45
 Ser Pro Asp Arg Ser Ser Ser Arg Gly Lys Lys Gln Arg Val Ser Gly
 50 55 60
 Cys Asn Asp Met Val Cys Phe Gly Phe Ser Gly Ala Ala Cys Leu Leu
 65 70 75 80
 Cys Gln Met Pro Val Phe Gly Gly Gly Phe Val Gly Phe Leu Pro Ser
 85 90 95
 Leu Phe Gln Thr
 100

<210> 83
 <211> 1533
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1533)

<400> 83
 atg gct tgg gca agt agg ctg ggc ctg ctg ctg gca ctg ctg ctg ccc
 Met Ala Trp Ala Ser Arg Leu Gly Leu Leu Leu Ala Leu Leu Leu Pro
 1 5 10 15

48

gtg gtc ggt gcc tcc acg cca ggc acc gtg gtc cga ctc aac aag gca Val Val Gly Ala Ser Thr Pro Gly Thr Val Val Arg Leu Asn Lys Ala 20 25 30	96
gca ttg agc tac gtg tct gaa att ggg aaa gcc cct ctc cag cgg gcc Ala Leu Ser Tyr Val Ser Glu Ile Gly Lys Ala Pro Leu Gln Arg Ala 35 40 45	144
ctg cag gtc act gtc cct cat ttc ctg gac tgg agt gga gag gcg ctt Leu Gln Val Thr Val Pro His Phe Leu Asp Trp Ser Gly Glu Ala Leu 50 55 60	192
cag ccc acc agg atc cgg att ctg aat gtc cat gtg ccc cgc ctc cac Gln Pro Thr Arg Ile Arg Ile Leu Asn Val His Val Pro Arg Leu His 65 70 75 80	240
ctg aaa ttc att gct ggt ttc gga gtg cgc ctg ctg gca gca gct aat Leu Lys Phe Ile Ala Gly Phe Gly Val Arg Leu Leu Ala Ala Ala Asn 85 90 95	288
ttt act ttc aag gtc ttt cgc gcc cca gag ccc ctg gag ctg acg ctg Phe Thr Phe Lys Val Phe Arg Ala Pro Glu Pro Leu Glu Leu Thr Leu 100 105 110	336
cct gtg gaa ctg ctg gct gac acc cgc gtg acc cag agc tcc atc agg Pro Val Glu Leu Leu Ala Asp Thr Arg Val Thr Gln Ser Ser Ile Arg 115 120 125	384
acc cct gtg gtc agc atc tct gcc tgc tct tta ttc tcg ggc cac gcc Thr Pro Val Val Ser Ile Ser Ala Cys Ser Leu Phe Ser Gly His Ala 130 135 140	432
aac gag ttt gat ggc agt aac agc acc tcc cac gcg ctg ctg gtc ctg Asn Glu Phe Asp Gly Ser Asn Ser Thr Ser His Ala Leu Leu Val Leu 145 150 155 160	480
gtg cag aag cac att aaa gct gtc ttg agt aac aag ctg tgc ctg agc Val Gln Lys His Ile Lys Ala Val Leu Ser Asn Lys Leu Cys Leu Ser 165 170 175	528
atc tcc aac ctg gtg cag ggt gtc aat gtc cac ctg ggc acc tta att Ile Ser Asn Leu Val Gln Gly Val Asn Val His Leu Gly Thr Leu Ile 180 185 190	576

Met 1	Ala	Trp	Ala	Ser 5	Arg	Leu	Gly	Leu	Leu 10	Leu	Ala	Leu	Leu	Leu 15	Pro
Val	Val	Gly	Ala 20	Ser	Thr	Pro	Gly	Thr	Val	Val	Arg	Leu	Asn 30	Lys	Ala
Ala	Leu	Ser	Tyr	Val	Ser	Glu	Ile 40	Gly	Lys	Ala	Pro	Leu	Gln	Arg	Ala
Leu	Gln 50	Val	Thr	Val	Pro	His 55	Phe	Leu	Asp	Trp	Ser 60	Gly	Glu	Ala	Leu
Gln 65	Pro	Thr	Arg	Ile	Arg	Ile 70	Leu	Asn	Val	His 75	Val	Pro	Arg	Leu	His
Leu	Lys	Phe	Ile	Ala 85	Gly	Phe	Gly	Val	Arg 90	Leu	Leu	Ala	Ala	Ala 95	Asn
Phe	Thr	Phe	Lys 100	Val	Phe	Arg	Ala	Pro 105	Glu	Pro	Leu	Glu	Leu	Thr	Leu
Pro	Val	Glu	Leu	Leu	Ala	Asp	Thr	Arg	Val	Thr	Gln	Ser	Ser	Ile	Arg
Thr	Pro 130	Val	Val	Ser	Ile	Ser 135	Ala	Cys	Ser	Leu	Phe 140	Ser	Gly	His	Ala
Asn 145	Glu	Phe	Asp	Gly	Ser	Asn 150	Ser	Thr	Ser	His 155	Ala	Leu	Leu	Val	Leu
Val	Gln	Lys	His	Ile 165	Lys	Ala	Val	Leu	Ser	Asn 170	Lys	Leu	Cys	Leu	Ser
Ile	Ser	Asn	Leu 180	Val	Gln	Gly	Val	Asn 185	Val	His	Leu	Gly	Thr	Leu	Ile
Gly	Leu	Asn 195	Pro	Val	Gly	Pro	Glu 200	Ser	Gln	Ile	Arg	Tyr 205	Ser	Met	Val
Ser	Val 210	Pro	Thr	Val	Thr	Ser	Asp 215	Tyr	Ile	Ser	Leu	Glu	Val	Asn	Ala
Val 225	Leu	Phe	Leu	Leu	Gly	Lys 230	Pro	Ile	Ile	Leu	Pro	Thr	Asp	Ala	Thr
Pro	Phe	Val	Leu	Pro	Arg	His 245	Val	Gly	Thr	Glu	Gly	Ser	Met	Ala	Thr
Val	Gly	Leu	Ser 260	Gln	Gln	Leu	Phe	Asp 265	Ser	Ala	Leu	Leu	Leu	Leu	Gln
Lys	Ala	Gly	Ala 275	Leu	Asn	Leu	Asp 280	Ile	Thr	Gly	Gln	Leu	Val	Ala	Arg
Gln	Phe 290	Pro	Glu	Pro	Met	Pro 295	Val	Val	Leu	Lys	Val 300	Arg	Leu	Gly	Ala
Thr 305	Pro	Val	Ala	Met	Leu	His 310	Thr	Asn	Asn	Ala	Thr	Leu	Arg	Leu	Gln
Pro	Phe	Val	Glu	Val	Leu	Ala	Thr	Ala	Ser	Asn	Ser	Ala	Phe	Gln	Ser

Leu Pro Ala His Ser Asn Glu Arg Lys Leu Arg Gly Ser Pro Gln Val
 35 40 45
 cca gcc aag tct tca gag ccg gcc act ctg gcc aac agc ttg agt aca 192
 Pro Ala Lys Ser Ser Glu Pro Ala Thr Leu Ala Asn Ser Leu Ser Thr
 50 55 60
 act gca cgc aag ccg caa gcc gga acc act ggg cta gga tgc tcc cag 240
 Thr Ala Arg Lys Pro Gln Ala Gly Thr Thr Gly Leu Gly Cys Ser Gln
 65 70 75 80
 att ctg agc tct gag gat ttg act cag gca aag att att gct gct ggc 288
 Ile Leu Ser Ser Glu Asp Leu Thr Gln Ala Lys Ile Ile Ala Ala Gly
 85 90 95
 aga agg tcg agg caa aaa ttc tct acc ttg gag gga agg gtg gat aca 336
 Arg Arg Ser Arg Gln Lys Phe Ser Thr Leu Glu Gly Arg Val Asp Thr
 100 105 110
 gat atc aaa cag atg tct agt ctt gct agg aat ggg gcc gaa aac tcc 384
 Asp Ile Lys Gln Met Ser Ser Leu Ala Arg Asn Gly Ala Glu Asn Ser
 115 120 125
 cac cct acg cca acc atg gac aca agg aga agt ttg gca gcc aca ggt 432
 His Pro Thr Pro Thr Met Asp Thr Arg Arg Ser Leu Ala Ala Thr Gly
 130 135 140
 aga agg agc aag aat gct tag 453
 Arg Arg Ser Lys Asn Ala *
 145 150

<210> 86

<211> 150

<212> PRT

<213> Homo sapiens

<400> 86

Met Ala Val Leu Val Val Ser Leu Gly Ser Leu Ala Leu Gly Glu Glu
 1 5 10 15
 Val Leu Leu Val Ala Pro Trp Arg Gly Pro His Ser Lys Glu Leu Lys
 20 25 30
 Leu Pro Ala His Ser Asn Glu Arg Lys Leu Arg Gly Ser Pro Gln Val

35 40 45
 Pro Ala Lys Ser Ser Glu Pro Ala Thr Leu Ala Asn Ser Leu Ser Thr
 50 55 60
 Thr Ala Arg Lys Pro Gln Ala Gly Thr Thr Gly Leu Gly Cys Ser Gln
 65 70 75 80
 Ile Leu Ser Ser Glu Asp Leu Thr Gln Ala Lys Ile Ile Ala Ala Gly
 85 90 95
 Arg Arg Ser Arg Gln Lys Phe Ser Thr Leu Glu Gly Arg Val Asp Thr
 100 105 110
 Asp Ile Lys Gln Met Ser Ser Leu Ala Arg Asn Gly Ala Glu Asn Ser
 115 120 125
 His Pro Thr Pro Thr Met Asp Thr Arg Arg Ser Leu Ala Ala Thr Gly
 130 135 140
 Arg Arg Ser Lys Asn Ala
 145 150

<210> 87
 <211> 438
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(438)

<400> 87

atg ggc cgc cgc cgc ctg ctc gtc tgg ctg tgc gcc gtc gcg gcg ctg 48
 Met Gly Arg Arg Arg Leu Leu Val Trp Leu Cys Ala Val Ala Ala Leu
 1 5 10 15

ctc tcg ggg gcg cag gcc agg ggc acc ccg ctc ctg gcg cgg cct gcg 96
 Leu Ser Gly Ala Gln Ala Arg Gly Thr Pro Leu Leu Ala Arg Pro Ala
 20 25 30

ccg ccc ggt gcc tcc cgc tac agt ctc tac acg acg gga tgg cgc ccg 144
 Pro Pro Gly Ala Ser Arg Tyr Ser Leu Tyr Thr Thr Gly Trp Arg Pro
 35 40 45

cgg ctg cgc ccg ggg ccg cac aag gcc ctc tgt gcc tat gtg gtg cac 192
 Arg Leu Arg Pro Gly Pro His Lys Ala Leu Cys Ala Tyr Val Val His
 50 55 60

agg aat gtg acc tgc atc cta cag gag gga gcg gag agc tac gta aag 240

100 105 110
 Gly Ser Ala Ser His Ala Glu Tyr Arg Gly Ser His Asp Ser Ile Asn
 115 120 125
 Arg Gly Leu Gly Ser Leu Arg Cys Ala Arg Met Tyr Ala Gln Leu Val
 130 135 140
 Ile
 145

<210> 89
 <211> 372
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(372)

<400> 89

atg ctg ctg ctg ctc ctg ttg ctg ctg ctg cta cag ctc cag gcc ctt 48
 Met Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Gln Leu Gln Ala Leu
 1 5 10 15

gct ctg gtg cca ctg gag caa aat ctc tcc cca aga ccc cgg gtg aag 96
 Ala Leu Val Pro Leu Glu Gln Asn Leu Ser Pro Arg Pro Arg Val Lys
 20 25 30

agt gct gct cca aca caa caa cca gtc acc tgc ttg ctg agg att ggt 144
 Ser Ala Ala Pro Thr Gln Gln Pro Val Thr Cys Leu Leu Arg Ile Gly
 35 40 45

tgt cat gct cct gct tgg ccc aca agc atc tcc cac aag aaa ttc tgc 192
 Cys His Ala Pro Ala Trp Pro Thr Ser Ile Ser His Lys Lys Phe Cys
 50 55 60

agg aaa tcc agg gtc ctg tct gaa ccc aaa gat gtt tct atc tat cga 240
 Arg Lys Ser Arg Val Leu Ser Glu Pro Lys Asp Val Ser Ile Tyr Arg
 65 70 75 80

atg ttc cct ggt cat tgg ttg aag gcc atc aag tcg gcg gtg aaa gtc 288
 Met Phe Pro Gly His Trp Leu Lys Ala Ile Lys Ser Ala Val Lys Val
 85 90 95

tta ccc agt act tac aca gta ctt cag ctt agc tgc gaa aat atc aat 336

Leu Pro Ser Thr Tyr Thr Val Leu Gln Leu Ser Cys Glu Asn Ile Asn
 100 105 110

gag ctg ccg aac tgt gtg gac ccc aag cca ggc tga 372
 Glu Leu Pro Asn Cys Val Asp Pro Lys Pro Gly *
 115 120

<210> 90
 <211> 123
 <212> PRT
 <213> Homo sapiens

<400> 90
 Met Leu Leu Leu Leu Leu Leu Leu Leu Leu Gln Leu Gln Ala Leu
 1 5 10 15
 Ala Leu Val Pro Leu Glu Gln Asn Leu Ser Pro Arg Pro Arg Val Lys
 20 25 30
 Ser Ala Ala Pro Thr Gln Gln Pro Val Thr Cys Leu Leu Arg Ile Gly
 35 40 45
 Cys His Ala Pro Ala Trp Pro Thr Ser Ile Ser His Lys Lys Phe Cys
 50 55 60
 Arg Lys Ser Arg Val Leu Ser Glu Pro Lys Asp Val Ser Ile Tyr Arg
 65 70 75 80
 Met Phe Pro Gly His Trp Leu Lys Ala Ile Lys Ser Ala Val Lys Val
 85 90 95
 Leu Pro Ser Thr Tyr Thr Val Leu Gln Leu Ser Cys Glu Asn Ile Asn
 100 105 110
 Glu Leu Pro Asn Cys Val Asp Pro Lys Pro Gly
 115 120

<210> 91
 <211> 618
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(618)

<400> 91
 atg gag ttg ctg tta ctg gcg gtg ttg agt cgg ggg act ggg gca gtt 48
 Met Glu Leu Leu Leu Leu Ala Val Leu Ser Arg Gly Thr Gly Ala Val

1					5					10					15					
gca	ctg	ctg	tct	gac	tgc	att	ttc	aaa	ggg	cag	cag	tgc	tgt	gct	ggg			96		
Ala	Leu	Leu	Ser	Asp	Cys	Ile	Phe	Lys	Gly	Gln	Gln	Cys	Cys	Ala	Gly					
			20					25					30							
ggt	ctg	ctc	cag	tcc	cta	gtc	acc	tcg	tac	tcc	cta	aat	gct	gaa	ggc			144		
Gly	Leu	Leu	Gln	Ser	Leu	Val	Thr	Ser	Tyr	Ser	Leu	Asn	Ala	Glu	Gly					
			35					40					45							
aaa	caa	cag	cta	agg	ctg	caa	aac	agc	aaa	gat	gat	gac	ctg	ccc	ctc			192		
Lys	Gln	Gln	Leu	Arg	Leu	Gln	Asn	Ser	Lys	Asp	Asp	Asp	Leu	Pro	Leu					
50						55						60								
cct	ctg	gga	gct	cca	acc	cac	ggg	ggg	atg	ggg	ctg	ctg	aaa	aca	cca			240		
Pro	Leu	Gly	Ala	Pro	Thr	His	Gly	Gly	Met	Gly	Leu	Leu	Lys	Thr	Pro					
65				70						75				80						
gca	aag	ggt	gac	tgg	aga	ccc	tgg	tcc	tgc	cca	aat	tcg	gct	gtg	aat			288		
Ala	Lys	Gly	Asp	Trp	Arg	Pro	Trp	Ser	Cys	Pro	Asn	Ser	Ala	Val	Asn					
			85					90					95							
cca	tct	ggt	cct	gga	ctc	ttt	ttg	gtt	ggt	aaa	cta	ttg	att	att	gcc			336		
Pro	Ser	Gly	Pro	Gly	Leu	Phe	Leu	Val	Gly	Lys	Leu	Leu	Ile	Ile	Ala					
			100					105					110							
aca	att	tca	gag	cct	gtt	att	ggt	cta	ttc	aga	gat	tca	act	tct	tcc			384		
Thr	Ile	Ser	Glu	Pro	Val	Ile	Gly	Leu	Phe	Arg	Asp	Ser	Thr	Ser	Ser					
115						120					125									
tgg	ttt	agt	ctt	ggg	aga	gtg	tat	gtg	tcg	agg	aat	gta	tcc	att	tct			432		
Trp	Phe	Ser	Leu	Gly	Arg	Val	Tyr	Val	Ser	Arg	Asn	Val	Ser	Ile	Ser					
130						135				140										
tac	aac	gga	tgt	gaa	gga	cct	ctt	caa	gga	gaa	cta	caa	acc	act	gct			480		
Tyr	Asn	Gly	Cys	Glu	Gly	Pro	Leu	Gln	Gly	Glu	Leu	Gln	Thr	Thr	Ala					
145				150						155				160						
caa	gga	aat	aaa	aga	gga	cac	aaa	caa	atg	gaa	gaa	cat	tcc	atg	ctc			528		
Gln	Gly	Asn	Lys	Arg	Gly	His	Lys	Gln	Met	Glu	Glu	His	Ser	Met	Leu					
			165					170					175							
atg	ggt	agg	aag	aat	caa	tat	cgt	gaa	aat	ggc	cat	act	gcc	caa	gac			576		

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(342)

<400> 93

atg gcg gcg gcc cca cgc gcg ggc cgg cgg cgc ggg cag ccg ctc ctg	48
Met Ala Ala Ala Pro Arg Ala Gly Arg Arg Arg Gly Gln Pro Leu Leu	
1 5 10 15	

gcg ctg ctg ctt ctg ctg ctg gcg cca ctg ccg ccg ggg gcc ccg ccg	96
Ala Leu Leu Leu Leu Leu Leu Ala Pro Leu Pro Pro Gly Ala Pro Pro	
20 25 30	

ggc gcc gac gcc tac ttc ccc gag gag cgc tgg agc ccg gag tcg ccc	144
Gly Ala Asp Ala Tyr Phe Pro Glu Glu Arg Trp Ser Pro Glu Ser Pro	
35 40 45	

ctg cag gcg ccg cgc gtg ctc atc gcg ctg ttg gcg cga aac gcg gcc	192
Leu Gln Ala Pro Arg Val Leu Ile Ala Leu Leu Ala Arg Asn Ala Ala	
50 55 60	

cac gcg ttg ccc acc acg ctg ggc gca ctc gag cgg ctg cgg cac ccg	240
His Ala Leu Pro Thr Thr Leu Gly Ala Leu Glu Arg Leu Arg His Pro	
65 70 75 80	

cgg gag cgc acg gcg cta tgg acg gag ccc aga gcc ccc act ggg gcg	288
Arg Glu Arg Thr Ala Leu Trp Thr Glu Pro Arg Ala Pro Thr Gly Ala	
85 90 95	

ttg cca gag gcc aca tct aac agc aag cct ttc tgt gcc ggc tgc tgc	336
Leu Pro Glu Ala Thr Ser Asn Ser Lys Pro Phe Cys Ala Gly Cys Cys	
100 105 110	

cct taa	342
Pro *	

<210> 94

<211> 113

<212> PRT

<213> Homo sapiens

<400> 94

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Met Ala Ala Ala Pro Arg Ala Gly Arg Arg Arg Gly Gln Pro Leu Leu
 1      5      10      15
Ala Leu Leu Leu Leu Leu Ala Pro Leu Pro Pro Gly Ala Pro Pro
 20      25      30
Gly Ala Asp Ala Tyr Phe Pro Glu Glu Arg Trp Ser Pro Glu Ser Pro
 35      40      45
Leu Gln Ala Pro Arg Val Leu Ile Ala Leu Leu Ala Arg Asn Ala Ala
 50      55      60
His Ala Leu Pro Thr Thr Leu Gly Ala Leu Glu Arg Leu Arg His Pro
 65      70      75      80
Arg Glu Arg Thr Ala Leu Trp Thr Glu Pro Arg Ala Pro Thr Gly Ala
 85      90      95
Leu Pro Glu Ala Thr Ser Asn Ser Lys Pro Phe Cys Ala Gly Cys Cys
 100     105     110
Pro

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<210> 95

<211> 343

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(343)

<400> 95

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atg aca gca agc cgc cag atg ttt aga ctt tct gtt ctc ctt gct ggc      48
Met Thr Ala Ser Arg Gln Met Phe Arg Leu Ser Val Leu Leu Ala Gly
 1      5      10      15

tct gta ttg cca gcc ctg gct act gct gtt aga aac ctt tct gag act      96
Ser Val Leu Pro Ala Leu Ala Thr Ala Val Arg Asn Leu Ser Glu Thr
 20      25      30

aga cca gtt aaa ctt gtg gtt ccg tgg gtt gat atc cag aaa tta gaa      144
Arg Pro Val Lys Leu Val Val Pro Trp Val Asp Ile Gln Lys Leu Glu
 35      40      45

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[illegible]

<210> 97
 <211> 420
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(420)

<400> 97

atg	ctg	ctg	ctg	ctg	ctg	ttg	ttt	atg	aga	cag	ggt	ctg	gct	ctg	tca	48
Met	Leu	Leu	Leu	Leu	Leu	Leu	Phe	Met	Arg	Gln	Gly	Leu	Ala	Leu	Ser	
1				5					10					15		

ccc	agc	ctg	gag	tgc	agt	gac	gtc	atc	att	gcc	cac	tgc	agc	ctc	agc	96
Pro	Ser	Leu	Glu	Cys	Ser	Asp	Val	Ile	Ile	Ala	His	Cys	Ser	Leu	Ser	
			20					25					30			

ctc	gtg	ggc	tcg	agt	gat	cct	cct	gaa	aca	aca	tat	att	ggc	acc	ctc	144
Leu	Val	Gly	Ser	Ser	Asp	Pro	Pro	Glu	Thr	Thr	Tyr	Ile	Gly	Thr	Leu	
		35				40						45				

ctt	gtg	tct	gtg	aat	cca	tac	cag	gag	ctc	gga	atc	tac	act	gtg	ctg	192
Leu	Val	Ser	Val	Asn	Pro	Tyr	Gln	Glu	Leu	Gly	Ile	Tyr	Thr	Val	Leu	
	50					55					60					

tgc	aag	tcc	aag	aac	att	atc	ctg	agg	gaa	tgc	ttc	ctg	ctg	gcc	gag	240
Cys	Lys	Ser	Lys	Asn	Ile	Ile	Leu	Arg	Glu	Cys	Phe	Leu	Leu	Ala	Glu	
65				70					75					80		

tta	gaa	aac	cgg	agg	agg	ccc	cca	aca	ggc	ttg	tcc	aat	aag	ggt	gtg	288
Leu	Glu	Asn	Arg	Arg	Arg	Pro	Pro	Thr	Gly	Leu	Ser	Asn	Lys	Gly	Val	
			85					90						95		

gcc	tat	ctc	cct	act	gga	cct	ctt	ctg	gag	gga	gcc	tca	acg	ccc	aaa	336
Ala	Tyr	Leu	Pro	Thr	Gly	Pro	Leu	Leu	Glu	Gly	Ala	Ser	Thr	Pro	Lys	
			100				105						110			

aga	cct	aat	aac	aac	aat	aaa	att	gtg	ggc	aca	ttg	cca	atg	atg	gga	384
Arg	Pro	Asn	Asn	Asn	Asn	Lys	Ile	Val	Gly	Thr	Leu	Pro	Met	Met	Gly	
		115					120					125				

420

<400> 98

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<210> 99
<211> 2172
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (1)...(2172)

<400> 99

48

cct tct ctg ctg ctg ttg tta gag ggc aca cgc tgg caa gct ctg gtg 576
Pro Ser Leu Leu Leu Leu Leu Glu Gly Thr Arg Trp Gln Ala Leu Val

180	185	190	
cag gtg cag ccc agt gtg gac ccc acc aat gcc aca ggc ctc gat ggg Gln Val Gln Pro Ser Val Asp Pro Thr Asn Ala Thr Gly Leu Asp Gly 195 200 205			624
agg gag gca gct cct cac ttt ttg cag ggt ctg ttg ggt ttg ctt acc Arg Glu Ala Ala Pro His Phe Leu Gln Gly Leu Leu Gly Leu Leu Thr 210 215 220			672
cca aca ggg gag cta ggc tcc aag gag gct ctt tgg ggc ggt ctg cta Pro Thr Gly Glu Leu Gly Ser Lys Glu Ala Leu Trp Gly Gly Leu Leu 225 230 235 240			720
cgc aca gtg ggg gcc ccc ctc tat gct gcc ttt cag gag ggg ctg ctc Arg Thr Val Gly Ala Pro Leu Tyr Ala Ala Phe Gln Glu Gly Leu Leu 245 250 255			768
cgt gtc act cac tcc ctg cag gat gag gtc ttc tcc att ttg ggg cag Arg Val Thr His Ser Leu Gln Asp Glu Val Phe Ser Ile Leu Gly Gln 260 265 270			816
cca gag cct gat acc aat ggg cag tgc cag gga ggt aac ctt caa cag Pro Glu Pro Asp Thr Asn Gly Gln Cys Gln Gly Gly Asn Leu Gln Gln 275 280 285			864
ctg ctc tta tgg ggc gtc cgg cac aac ctt tcc tgg gat gtc cag gcg Leu Leu Leu Trp Gly Val Arg His Asn Leu Ser Trp Asp Val Gln Ala 290 295 300			912
ctg ggc ttt ctg tct gga tca cca ccc cca ccc cct gcc ctc ctt cac Leu Gly Phe Leu Ser Gly Ser Pro Pro Pro Pro Pro Ala Leu Leu His 305 310 315 320			960
tgc ctg agc acg ggc gtg cct ctg ccc aga gct tct cag ccg tca gcc Cys Leu Ser Thr Gly Val Pro Leu Pro Arg Ala Ser Gln Pro Ser Ala 325 330 335			1008
cac atc agc cca cgc caa cgg cga gcc atc act gtg gag gcc ctc tgt His Ile Ser Pro Arg Gln Arg Arg Ala Ile Thr Val Glu Ala Leu Cys 340 345 350			1056
gag aac cac tta ggc cca gca cca ccc tac agc att tcc aac ttc tcc			1104

Glu	Asn	His	Leu	Gly	Pro	Ala	Pro	Tyr	Ser	Ile	Ser	Asn	Phe	Ser		
		355					360				365					
atc	cac	ttg	ctc	tgc	cag	cac	acc	aag	cct	gcc	act	cca	cag	ccc	cat	1152
Ile	His	Leu	Leu	Cys	Gln	His	Thr	Lys	Pro	Ala	Thr	Pro	Gln	Pro	His	
	370					375					380					
ccc	agc	acc	act	gcc	atc	tgc	cag	aca	gct	gtg	tgg	tat	gca	gtg	tcc	1200
Pro	Ser	Thr	Thr	Ala	Ile	Cys	Gln	Thr	Ala	Val	Trp	Tyr	Ala	Val	Ser	
385					390					395					400	
tgg	gca	cca	ggc	gcc	caa	ggc	tgg	cta	cag	gcc	tgc	cac	gac	cag	ttt	1248
Trp	Ala	Pro	Gly	Ala	Gln	Gly	Trp	Leu	Gln	Ala	Cys	His	Asp	Gln	Phe	
			405					410						415		
cct	gat	gag	ttt	ttg	gat	gcg	atc	tgc	agt	aac	ctc	tcc	ttt	tca	gcc	1296
Pro	Asp	Glu	Phe	Leu	Asp	Ala	Ile	Cys	Ser	Asn	Leu	Ser	Phe	Ser	Ala	
			420					425					430			
ctg	tct	ggc	tcc	aac	cgc	cgc	ctg	gtg	aag	cgg	ctc	tgt	gct	ggc	ctg	1344
Leu	Ser	Gly	Ser	Asn	Arg	Arg	Leu	Val	Lys	Arg	Leu	Cys	Ala	Gly	Leu	
		435					440					445				
ctc	cca	ccc	cct	acc	agc	tgc	cct	gaa	ggc	ctg	ccc	cct	gtt	ccc	ctc	1392
Leu	Pro	Pro	Pro	Thr	Ser	Cys	Pro	Glu	Gly	Leu	Pro	Pro	Val	Pro	Leu	
	450					455					460					
acc	cca	gac	atc	ttt	tgg	ggc	tgc	ttc	ttg	gag	aat	gag	act	ctg	tgg	1440
Thr	Pro	Asp	Ile	Phe	Trp	Gly	Cys	Phe	Leu	Glu	Asn	Glu	Thr	Leu	Trp	
465					470					475				480		
gct	gag	cga	ctg	tgt	ggg	gag	gca	agt	cta	cag	gct	gtg	ccc	ccc	agc	1488
Ala	Glu	Arg	Leu	Cys	Gly	Glu	Ala	Ser	Leu	Gln	Ala	Val	Pro	Pro	Ser	
			485					490						495		
aac	cag	gct	tgg	gtc	cag	cat	gtg	tgc	cag	ggc	ccc	acc	cca	gat	gtc	1536
Asn	Gln	Ala	Trp	Val	Gln	His	Val	Cys	Gln	Gly	Pro	Thr	Pro	Asp	Val	
			500					505					510			
act	gcc	tcc	cca	cca	tgc	cac	att	gga	ccc	tgt	ggg	gaa	cgc	tgc	ccg	1584
Thr	Ala	Ser	Pro	Pro	Cys	His	Ile	Gly	Pro	Cys	Gly	Glu	Arg	Cys	Pro	
		515					520					525				

gat ggg ggc agc ttc ctg gtg atg gtc tgt gcc aat gac acc atg tat	1632
Asp Gly Gly Ser Phe Leu Val Met Val Cys Ala Asn Asp Thr Met Tyr	
530 535 540	
gag gtc ctg gtg ccc ttc tgg cct tgg cta gca ggc caa tgc agg ata	1680
Glu Val Leu Val Pro Phe Trp Pro Trp Leu Ala Gly Gln Cys Arg Ile	
545 550 555 560	
agt cgt ggg ggc aat gac act tgc ttc cta gaa ggg ctg ctg ggc ccc	1728
Ser Arg Gly Gly Asn Asp Thr Cys Phe Leu Glu Gly Leu Leu Gly Pro	
565 570 575	
ctt ctg ccc tct ctg cca cca ctg gga cca tcc cca ctc tgt ctg acc	1776
Leu Leu Pro Ser Leu Pro Pro Leu Gly Pro Ser Pro Leu Cys Leu Thr	
580 585 590	
cct ggc ccc ttc ctc ctt ggc atg cta tcc cag ttg cca cgc tgt cag	1824
Pro Gly Pro Phe Leu Leu Gly Met Leu Ser Gln Leu Pro Arg Cys Gln	
595 600 605	
tcc tct gtc cca gct ctt gct cac ccc aca cgc cta cac tat ctc ctc	1872
Ser Ser Val Pro Ala Leu Ala His Pro Thr Arg Leu His Tyr Leu Leu	
610 615 620	
cgc ctg ctg acc ttc ctc ttg ggt cca ggg gct ggg ggc gct gag gcc	1920
Arg Leu Leu Thr Phe Leu Leu Gly Pro Gly Ala Gly Gly Ala Glu Ala	
625 630 635 640	
cag ggg atg ctg ggt cgg gcc cta ctg ctc tcc agt ctc cca gac aac	1968
Gln Gly Met Leu Gly Arg Ala Leu Leu Leu Ser Ser Leu Pro Asp Asn	
645 650 655	
tgc tcc ttc tgg gat gcc ttt cgc cca gag ggc cgg cgc agt gtg cta	2016
Cys Ser Phe Trp Asp Ala Phe Arg Pro Glu Gly Arg Arg Ser Val Leu	
660 665 670	
cgg acg att ggg gaa tac ctg gaa caa gat gag gag cag cca acc cca	2064
Arg Thr Ile Gly Glu Tyr Leu Glu Gln Asp Glu Glu Gln Pro Thr Pro	
675 680 685	
tca ggc ttt gaa ccc act gtc aac ccc agc tct ggt ata agc aag atg	2112
Ser Gly Phe Glu Pro Thr Val Asn Pro Ser Ser Gly Ile Ser Lys Met	
690 695 700	

gag ctg ctg gcc tgc ttt agt gtg agt gct ctg cca gag gga aag ctc 2160
 Glu Leu Leu Ala Cys Phe Ser Val Ser Ala Leu Pro Glu Gly Lys Leu
 705 710 715 720

cta gaa cag tga 2172
 Leu Glu Gln *

<210> 100
 <211> 723
 <212> PRT
 <213> Homo sapiens

<400> 100
 Met Ala Leu Ser Leu Trp Pro Leu Leu Leu Leu Leu Leu Leu Leu Leu
 1 5 10 15
 Leu Leu Ser Phe Ala Val Thr Leu Ala Pro Thr Gly Pro His Ser Leu
 20 25 30
 Asp Pro Gly Leu Ser Phe Leu Lys Ser Leu Leu Ser Thr Leu Asp Gln
 35 40 45
 Ala Pro Gln Gly Ser Leu Ser Arg Ser Arg Phe Phe Thr Phe Leu Ala
 50 55 60
 Asn Ile Ser Ser Ser Phe Glu Pro Gly Arg Met Gly Glu Gly Pro Val
 65 70 75 80
 Gly Glu Pro Pro Pro Leu Gln Pro Pro Ala Leu Arg Leu His Asp Phe
 85 90 95
 Leu Val Thr Leu Arg Gly Ser Pro Asp Trp Glu Pro Met Leu Gly Leu
 100 105 110
 Leu Gly Asp Met Leu Ala Leu Leu Gly Gln Glu Gln Thr Pro Arg Asp
 115 120 125
 Phe Leu Val His Gln Ala Gly Val Leu Gly Gly Leu Val Glu Val Leu
 130 135 140
 Leu Gly Ala Leu Val Pro Gly Gly Pro Pro Thr Pro Thr Arg Pro Pro
 145 150 155 160
 Cys Thr Arg Asp Gly Pro Ser Asp Cys Val Leu Ala Ala Asp Trp Leu
 165 170 175
 Pro Ser Leu Leu Leu Leu Leu Glu Gly Thr Arg Trp Gln Ala Leu Val
 180 185 190
 Gln Val Gln Pro Ser Val Asp Pro Thr Asn Ala Thr Gly Leu Asp Gly
 195 200 205
 Arg Glu Ala Ala Pro His Phe Leu Gln Gly Leu Leu Gly Leu Leu Thr

210	215	220
Pro Thr Gly Glu Leu Gly Ser Lys Glu Ala Leu Trp Gly Gly Leu Leu		
225	230	235
Arg Thr Val Gly Ala Pro Leu Tyr Ala Ala Phe Gln Glu Gly Leu Leu		
	245	250
Arg Val Thr His Ser Leu Gln Asp Glu Val Phe Ser Ile Leu Gly Gln		
	260	265
Pro Glu Pro Asp Thr Asn Gly Gln Cys Gln Gly Gly Asn Leu Gln Gln		
	275	280
Leu Leu Leu Trp Gly Val Arg His Asn Leu Ser Trp Asp Val Gln Ala		
	290	295
Leu Gly Phe Leu Ser Gly Ser Pro Pro Pro Pro Pro Ala Leu Leu His		
305	310	315
Cys Leu Ser Thr Gly Val Pro Leu Pro Arg Ala Ser Gln Pro Ser Ala		
	325	330
His Ile Ser Pro Arg Gln Arg Arg Ala Ile Thr Val Glu Ala Leu Cys		
	340	345
Glu Asn His Leu Gly Pro Ala Pro Pro Tyr Ser Ile Ser Asn Phe Ser		
	355	360
Ile His Leu Leu Cys Gln His Thr Lys Pro Ala Thr Pro Gln Pro His		
	370	375
Pro Ser Thr Thr Ala Ile Cys Gln Thr Ala Val Trp Tyr Ala Val Ser		
385	390	395
Trp Ala Pro Gly Ala Gln Gly Trp Leu Gln Ala Cys His Asp Gln Phe		
	405	410
Pro Asp Glu Phe Leu Asp Ala Ile Cys Ser Asn Leu Ser Phe Ser Ala		
	420	425
Leu Ser Gly Ser Asn Arg Arg Leu Val Lys Arg Leu Cys Ala Gly Leu		
	435	440
Leu Pro Pro Pro Thr Ser Cys Pro Glu Gly Leu Pro Pro Val Pro Leu		
	450	455
Thr Pro Asp Ile Phe Trp Gly Cys Phe Leu Glu Asn Glu Thr Leu Trp		
465	470	475
Ala Glu Arg Leu Cys Gly Glu Ala Ser Leu Gln Ala Val Pro Pro Ser		
	485	490
Asn Gln Ala Trp Val Gln His Val Cys Gln Gly Pro Thr Pro Asp Val		
	500	505
Thr Ala Ser Pro Pro Cys His Ile Gly Pro Cys Gly Glu Arg Cys Pro		
	515	520
Asp Gly Gly Ser Phe Leu Val Met Val Cys Ala Asn Asp Thr Met Tyr		
	530	535
Glu Val Leu Val Pro Phe Trp Pro Trp Leu Ala Gly Gln Cys Arg Ile		
545	550	555
		560

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<210> 101
<211> 456
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (1)...(456)
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atg ctg agc agc cag tat ggg ctg atc gtg ttc gtg gcg ggg ctg ctg 48
Met Leu Ser Ser Gln Tyr Gly Leu Ile Val Phe Val Ala Gly Leu Leu
1 5 10 15

ctg ctg ctg gcc tgg gcc gtt cga ccg cgg gca tgc tgt ggt acg tgg 96
Leu Leu Leu Ala Trp Ala Val Arg Pro Arg Ala Cys Cys Gly Thr Trp
20 25 30

gcc gca ctc cgg aac cgc cgc ctc ttc cgc ctc aag gac acg cac gcc 144
Ala Ala Leu Arg Asn Arg Arg Leu Phe Arg Leu Lys Asp Thr His Ala

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<210> 102
<211> 151
<212> PRT
<213> Homo sapiens
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<400>															102
Met	Leu	Ser	Ser	Gln	Tyr	Gly	Leu	Ile	Val	Phe	Val	Ala	Gly	Leu	Leu
1				5				10						15	
Leu	Leu	Leu	Ala	Trp	Ala	Val	Arg	Pro	Arg	Ala	Cys	Cys	Gly	Thr	Trp
			20					25					30		
Ala	Ala	Leu	Arg	Asn	Arg	Arg	Leu	Phe	Arg	Leu	Lys	Asp	Thr	His	Ala
		35					40					45			

Gly Ala Gly Trp Leu His Arg Leu Glu Pro Pro Leu Arg Leu Gln Thr
 50 55 60
 Leu Pro Ser Leu Gln Pro Gln Leu Gln Lys Pro Leu Leu Ser Phe Pro
 65 70 75 80
 Gly Leu Lys Pro Tyr Ser Gly Pro Thr Asp Pro Met Arg Glu Phe Ser
 85 90 95
 Ser Val Ala Asp Val Leu Trp Leu Gln Ala Ala Lys Cys Cys Phe Pro
 100 105 110
 Leu Leu Val Lys Glu Pro Ser Asn Pro Ser Asp Leu Pro Ser Arg Ala
 115 120 125
 Arg Ser Gly Pro Ser Ser Asn His Leu Gly Ala Ala Gly Arg Leu Leu
 130 135 140
 Tyr Ser Ala Arg Lys Glu Glu
 145 150

<210> 103
 <211> 414
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(414)

<400> 103

atg ggg cga gtc cgg acc ttg gcg ggc gag tgc tcg gcg cag gcg caa 48
 Met Gly Arg Val Arg Thr Leu Ala Gly Glu Cys Ser Ala Gln Ala Gln
 1 5 10 15

gcg cag agt ctc ctc gcg gtc gtc ctt ttg gcc cct ccc ctc tgg ggg 96
 Ala Gln Ser Leu Leu Ala Val Val Leu Leu Ala Pro Pro Leu Trp Gly
 20 25 30

acc ccc agt gcc agg ctg tca gtg cgc agc ccc cag cct gcg gga ccc 144
 Thr Pro Ser Ala Arg Leu Ser Val Arg Ser Pro Gln Pro Ala Gly Pro
 35 40 45

ctg ggg act ctg ggc gcc tgt tct gca aat gac cgg ttc tta cga gtt 192
 Leu Gly Thr Leu Gly Ala Cys Ser Ala Asn Asp Arg Phe Leu Arg Val
 50 55 60

caa gct gaa cca gcc acc cga gga tgg cat ctc ctc cgt gaa gtt aag 240
 Gln Ala Glu Pro Ala Thr Arg Gly Trp His Leu Leu Arg Glu Val Lys

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<210> 104
<211> 137
<212> PRT
<213> Homo sapiens

      <400> 104
Met Gly Arg Val Arg Thr Leu Ala Gly Glu Cys Ser Ala Gln Ala Gln
 1              5              10              15
Ala Gln Ser Leu Leu Ala Val Val Leu Leu Ala Pro Pro Leu Trp Gly
      20              25              30
Thr Pro Ser Ala Arg Leu Ser Val Arg Ser Pro Gln Pro Ala Gly Pro
      35              40              45
Leu Gly Thr Leu Gly Ala Cys Ser Ala Asn Asp Arg Phe Leu Arg Val
      50              55              60
Gln Ala Glu Pro Ala Thr Arg Gly Trp His Leu Leu Arg Glu Val Lys
65              70              75              80
Pro Pro His Pro Ser Gln Ser Trp Val Val Ser Phe Leu Gly Asp Val
      85              90              95
Pro Cys Val Phe Thr Met Trp Pro Gly Asn Phe Met Ala Val Lys Tyr
      100              105              110
Gln Ala His Arg Gly Pro Ser Trp Glu Trp Ala Phe Leu Ile Ser Ile
      115              120              125
Tyr Pro Leu Gly Arg Arg Val Lys Cys
      130              135

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<210> 105
 <211> 1260
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1260)

<400> 105

atg ggg ccc atg ctg ctg cct ctg gct ctg ctg gcc ctg ctg ctg ggg	48
Met Gly Pro Met Leu Leu Pro Leu Ala Leu Leu Ala Leu Leu Leu Gly	
1 5 10 15	
cct gcg ctg gcc cgg agt gcc cgg gac ccg gag gtg ttc tgt gga ggc	96
Pro Ala Leu Ala Arg Ser Ala Arg Asp Pro Glu Val Phe Cys Gly Gly	
20 25 30	
gtc ata tta gca ata aaa tgc atg aaa cca gca ttc ttt gcc acc ttc	144
Val Ile Leu Ala Ile Lys Cys Met Lys Pro Ala Phe Phe Ala Thr Phe	
35 40 45	
tcg cta atc att gct att ttc tcg gag aga gag gct ctt ggc aaa ggt	192
Ser Leu Ile Ile Ala Ile Phe Ser Glu Arg Glu Ala Leu Gly Lys Gly	
50 55 60	
cac agc cct gga ccc ggt ttt cct tcc tgg aat att tgg gtg gtg aca	240
His Ser Pro Gly Pro Gly Phe Pro Ser Trp Asn Ile Trp Val Val Thr	
65 70 75 80	
tcg cag ctg agc ccc ttc cat gga att ctg tgg tgt tgg gct gtt ctt	288
Ser Gln Leu Ser Pro Phe His Gly Ile Leu Trp Cys Trp Ala Val Leu	
85 90 95	
caa gag aag att agg aca cag aca cac aca gag gga cgg cca cgt gag	336
Gln Glu Lys Ile Arg Thr Gln Thr His Thr Glu Gly Arg Pro Arg Glu	
100 105 110	
gac ata ggg aga aga cag ctg tct gca agt caa gga ggg gcc tca gaa	384
Asp Ile Gly Arg Arg Gln Leu Ser Ala Ser Gln Gly Gly Ala Ser Glu	
115 120 125	

gga acc aac cct cct gac acc ttg atc ttg gac ttc cag ctg cag aac	432
Gly Thr Asn Pro Pro Asp Thr Leu Ile Leu Asp Phe Gln Leu Gln Asn	
130 135 140	
ggg tgt ttt ggc aaa tac acc ttc atc tgc tct tca cct ggt aaa tgc	480
Gly Cys Phe Gly Lys Tyr Thr Phe Ile Cys Ser Ser Pro Gly Lys Cys	
145 150 155 160	
ctg atc atc ttt cag gtc cta ctt gtc atg ctc tta ggg aag cct ccc	528
Leu Ile Ile Phe Gln Val Leu Leu Val Met Leu Leu Gly Lys Pro Pro	
165 170 175	
gtg ttc ttt gac aag aag gtc ccg tgc gtg gat caa ggc cct ccc tac	576
Val Phe Phe Asp Lys Lys Val Pro Ser Val Asp Gln Gly Pro Pro Tyr	
180 185 190	
tcc agt atg act tgg tct gaa tca atc cca tct gca aag acc cta ttc	624
Ser Ser Met Thr Trp Ser Glu Ser Ile Pro Ser Ala Lys Thr Leu Phe	
195 200 205	
cca aat aag gcc aca ttc aca gcg tgc agg gcg ctg atg gac gag ata	672
Pro Asn Lys Ala Thr Phe Thr Ala Cys Arg Ala Leu Met Asp Glu Ile	
210 215 220	
gag cac gac atc acc aag gct cgg cag aag aag acc aag gtg gga tcc	720
Glu His Asp Ile Thr Lys Ala Arg Gln Lys Lys Thr Lys Val Gly Ser	
225 230 235 240	
ttc cga atc aat ccc gat ggg act cag gag agg aga aag cac cta aat	768
Phe Arg Ile Asn Pro Asp Gly Thr Gln Glu Arg Arg Lys His Leu Asn	
245 250 255	
ttt gtg tct cgt caa gtc gaa aga cat ttc ggc act gtt ctt cat cag	816
Phe Val Ser Arg Gln Val Glu Arg His Phe Gly Thr Val Leu His Gln	
260 265 270	
aat aaa aat agc gcg tct gtg gtt ctt ggc aca ctc aag gat gga tcc	864
Asn Lys Asn Ser Ala Ser Val Val Leu Gly Thr Leu Lys Asp Gly Ser	
275 280 285	
ttc aag agc cgt gtc tgg caa gtc cac cgg agg gac ccc gtg cag gcc	912
Phe Lys Ser Arg Val Trp Gln Val His Arg Arg Asp Pro Val Gln Ala	
290 295 300	

cac tgg ctg ctc tgc tgc agg tct gac gcc tgc acc ccg gaa tct caa 960
 His Trp Leu Leu Cys Cys Arg Ser Asp Ala Cys Thr Pro Glu Ser Gln
 305 310 315 320

ggt cct ttg tgg tca cct gaa tgc agg aca tgt gcc tcc ata aaa tcc 1008
 Gly Pro Leu Trp Ser Pro Glu Cys Arg Thr Cys Ala Ser Ile Lys Ser
 325 330 335

agt aca gtc ctg gtc cct gac acc agc cgg gag ctg att ccc act gtc 1056
 Ser Thr Val Leu Val Pro Asp Thr Ser Arg Glu Leu Ile Pro Thr Val
 340 345 350

aag cag ggc cag gga aga tca ttc cgg gtc tac atg tgg tgt gga cta 1104
 Lys Gln Gly Gln Gly Arg Ser Phe Arg Val Tyr Met Trp Cys Gly Leu
 355 360 365

ggg gag gaa ttc ttc ccc cat agg agc tca cac tct gac cca gag acc 1152
 Gly Glu Glu Phe Phe Pro His Arg Ser Ser His Ser Asp Pro Glu Thr
 370 375 380

tca gca gcc gcc agt gtg aac gcc acg tct cag aga gtg aag gga ggg 1200
 Ser Ala Ala Ala Ser Val Asn Ala Thr Ser Gln Arg Val Lys Gly Gly
 385 390 395 400

agc ctc agg aaa tac act gag aca ata gtc aca gtt ctt gta tct gcg 1248
 Ser Leu Arg Lys Tyr Thr Glu Thr Ile Val Thr Val Leu Val Ser Ala
 405 410 415

tat tac tgc tga 1260
 Tyr Tyr Cys *

<210> 106

<211> 419

<212> PRT

<213> Homo sapiens

<400> 106

Met Gly Pro Met Leu Leu Pro Leu Ala Leu Leu Ala Leu Leu Leu Gly
 1 5 10 15
 Pro Ala Leu Ala Arg Ser Ala Arg Asp Pro Glu Val Phe Cys Gly Gly

Gly Glu Glu Phe Phe Pro His Arg Ser Ser His Ser Asp Pro Glu Thr
 370 375 380
 Ser Ala Ala Ala Ser Val Asn Ala Thr Ser Gln Arg Val Lys Gly Gly
 385 390 395 400
 Ser Leu Arg Lys Tyr Thr Glu Thr Ile Val Thr Val Leu Val Ser Ala
 405 410 415
 Tyr Tyr Cys

<210> 107
 <211> 669
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(669)

<400> 107

atg gcg cct cct ctg cga ccc ctc gcc cgg ctg cga ccg ccg ggg atg 48
 Met Ala Pro Pro Leu Arg Pro Leu Ala Arg Leu Arg Pro Pro Gly Met
 1 5 10 15

ctg ctc cgc gcg ctc ctg ctc ctg ctg ctg ctc agt cct ttg cca ggg 96
 Leu Leu Arg Ala Leu Leu Leu Leu Leu Leu Ser Pro Leu Pro Gly
 20 25 30

ctg cga gag gga ata ggt gaa ctc ata acc cca atc ggc acc agc ttg 144
 Leu Arg Glu Gly Ile Gly Glu Leu Ile Thr Pro Ile Gly Thr Ser Leu
 35 40 45

ccg gat ctg gat cca gcc agg agg aga tgg gag ggt gga att ggc agg 192
 Pro Asp Leu Asp Pro Ala Arg Arg Arg Trp Glu Gly Gly Ile Gly Arg
 50 55 60

gtt gga agt gaa gtg gcc gat ttg tgc ccc gga aag gag ggg gga aaa 240
 Val Gly Ser Glu Val Ala Asp Leu Cys Pro Gly Lys Glu Gly Gly Lys
 65 70 75 80

gtc ccc gaa gct gaa aag gaa gga gtg tgg tgc ttt agc gaa ctg tct 288
 Val Pro Glu Ala Glu Lys Glu Gly Val Trp Cys Phe Ser Glu Leu Ser
 85 90 95

ttt gta aaa gaa cca cag gat gta act gtc aca aga aag gac cca gtc 336
 Phe Val Lys Glu Pro Gln Asp Val Thr Val Thr Arg Lys Asp Pro Val
 100 105 110

gtt tta gat tgc cag gct cac gga gaa gtt cct att aag gtc aca tgg 384
 Val Leu Asp Cys Gln Ala His Gly Glu Val Pro Ile Lys Val Thr Trp
 115 120 125

ttg aaa aat gga gca aaa atg tct gaa aat aaa cgg atc gag gtt ctt 432
 Leu Lys Asn Gly Ala Lys Met Ser Glu Asn Lys Arg Ile Glu Val Leu
 130 135 140

tct aac ggc tct tta tac atc agt gag gtg gaa ggc agg cga gga gag 480
 Ser Asn Gly Ser Leu Tyr Ile Ser Glu Val Glu Gly Arg Arg Gly Glu
 145 150 155 160

cag tcc gat gaa gga ttt tat cag tgc ttg gca atg aac aaa tat gga 528
 Gln Ser Asp Glu Gly Phe Tyr Gln Cys Leu Ala Met Asn Lys Tyr Gly
 165 170 175

gcc att ctt agt caa aaa gct cat ctt gcc tta tca atg tta gcg gca 576
 Ala Ile Leu Ser Gln Lys Ala His Leu Ala Leu Ser Met Leu Ala Ala
 180 185 190

tcc ctg gcc tct acc ctc cca ata ccg ata gac tct ctt cca gtt gtg 624
 Ser Leu Ala Ser Thr Leu Pro Ile Pro Ile Asp Ser Leu Pro Val Val
 195 200 205

aca acc aag aaa gtt cta ctg tgg ggc aaa ata act cct gat tga 669
 Thr Thr Lys Lys Val Leu Leu Trp Gly Lys Ile Thr Pro Asp *
 210 215 220

<210> 108

<211> 222

<212> PRT

<213> Homo sapiens

<400> 108

Met Ala Pro Pro Leu Arg Pro Leu Ala Arg Leu Arg Pro Pro Gly Met
 1 5 10 15

Leu Leu Arg Ala Leu Leu Leu Leu Leu Leu Leu Ser Pro Leu Pro Gly
 20 25 30

Leu Arg Glu Gly Ile Gly Glu Leu Ile Thr Pro Ile Gly Thr Ser Leu
 35 40 45
 Pro Asp Leu Asp Pro Ala Arg Arg Arg Trp Glu Gly Gly Ile Gly Arg
 50 55 60
 Val Gly Ser Glu Val Ala Asp Leu Cys Pro Gly Lys Glu Gly Gly Lys
 65 70 75 80
 Val Pro Glu Ala Glu Lys Glu Gly Val Trp Cys Phe Ser Glu Leu Ser
 85 90 95
 Phe Val Lys Glu Pro Gln Asp Val Thr Val Thr Arg Lys Asp Pro Val
 100 105 110
 Val Leu Asp Cys Gln Ala His Gly Glu Val Pro Ile Lys Val Thr Trp
 115 120 125
 Leu Lys Asn Gly Ala Lys Met Ser Glu Asn Lys Arg Ile Glu Val Leu
 130 135 140
 Ser Asn Gly Ser Leu Tyr Ile Ser Glu Val Glu Gly Arg Arg Gly Glu
 145 150 155 160
 Gln Ser Asp Glu Gly Phe Tyr Gln Cys Leu Ala Met Asn Lys Tyr Gly
 165 170 175
 Ala Ile Leu Ser Gln Lys Ala His Leu Ala Leu Ser Met Leu Ala Ala
 180 185 190
 Ser Leu Ala Ser Thr Leu Pro Ile Pro Ile Asp Ser Leu Pro Val Val
 195 200 205
 Thr Thr Lys Lys Val Leu Leu Trp Gly Lys Ile Thr Pro Asp
 210 215 220

<210> 109
 <211> 864
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(864)

<400> 109

atg	cgg	caa	acc	cta	ccg	ctg	ctg	ctg	ctg	acg	gtg	ctg	cgc	ccc	agc	48
Met	Arg	Gln	Thr	Leu	Pro	Leu	Leu	Leu	Leu	Thr	Val	Leu	Arg	Pro	Ser	
1				5				10						15		
tgg	gca	gac	cct	ccc	cag	gag	aag	gtc	ccg	ctc	ttc	cgg	gtc	act	cag	96
Trp	Ala	Asp	Pro	Pro	Gln	Glu	Lys	Val	Pro	Leu	Phe	Arg	Val	Thr	Gln	
			20					25					30			

cag ggc ccc tgg ggg agc agt ggc agc aac gcc acc gac tcg ccc tgc 144
 Gln Gly Pro Trp Gly Ser Ser Gly Ser Asn Ala Thr Asp Ser Pro Cys
 35 40 45

gag ggg ctg ccc gcc gcg gat gcg acg gcc ttg acc ctg gcg aac cgc 192
 Glu Gly Leu Pro Ala Ala Asp Ala Thr Ala Leu Thr Leu Ala Asn Arg
 50 55 60

aac ctg gag cgc ctg ccc ggc tgc cta ccg cgc aca ctg cgc agc ctc 240
 Asn Leu Glu Arg Leu Pro Gly Cys Leu Pro Arg Thr Leu Arg Ser Leu
 65 70 75 80

gac gcc agc cac aac ctg ctg cgc gcc ctg agc act tcc gag ctc ggc 288
 Asp Ala Ser His Asn Leu Leu Arg Ala Leu Ser Thr Ser Glu Leu Gly
 85 90 95

cac ctg gag cag ctg cag gtg ctg acc ctg cgc cac aac cgc atc gcc 336
 His Leu Glu Gln Leu Gln Val Leu Thr Leu Arg His Asn Arg Ile Ala
 100 105 110

gcg ctg cgc tgg ggc ccg ggt ggg ccg gcg ggg ctg cac acc ctg gac 384
 Ala Leu Arg Trp Gly Pro Gly Gly Pro Ala Gly Leu His Thr Leu Asp
 115 120 125

ctc agc tac aac cag ctg gcc gct ctg ccg ccg tgc acc ggg ccc gcg 432
 Leu Ser Tyr Asn Gln Leu Ala Ala Leu Pro Pro Cys Thr Gly Pro Ala
 130 135 140

ctg agc agc ctc cgc gcc ctg gcg ctc gcc ggg aat ccg ctg cgg gcg 480
 Leu Ser Ser Leu Arg Ala Leu Ala Leu Ala Gly Asn Pro Leu Arg Ala
 145 150 155 160

ctg cag ccc cgg gcc ttc gcc tgc ttc ccc gcg ctg cag ctc ctc aac 528
 Leu Gln Pro Arg Ala Phe Ala Cys Phe Pro Ala Leu Gln Leu Leu Asn
 165 170 175

ctc tcc tgc acc gcg ctg ggt cgc gga gcc cag ggg ggc atc gcc gag 576
 Leu Ser Cys Thr Ala Leu Gly Arg Gly Ala Gln Gly Gly Ile Ala Glu
 180 185 190

gcg gcg ttc gct gga gag gat ggc gcg ccc ctg gtc acg ctc gaa gtc 624
 Ala Ala Phe Ala Gly Glu Asp Gly Ala Pro Leu Val Thr Leu Glu Val
 195 200 205

ctg gat ctc agc ggc acg ttc ctt gaa cgg gtt gag tca ggg tgg atc 672
 Leu Asp Leu Ser Gly Thr Phe Leu Glu Arg Val Glu Ser Gly Trp Ile
 210 215 220

aga gac ctg ccg aag ctc aca tcc ctc tac ctg agg aag atg cct cgg 720
 Arg Asp Leu Pro Lys Leu Thr Ser Leu Tyr Leu Arg Lys Met Pro Arg
 225 230 235 240

ctg acg acc ctg gag ggg gac att ttc aag atg acc ccc aac ctg cag 768
 Leu Thr Thr Leu Glu Gly Asp Ile Phe Lys Met Thr Pro Asn Leu Gln
 245 250 255

cag ctg gac tgt cag gac tcc cca gca ctt gct tct gtc gcc aca cac 816
 Gln Leu Asp Cys Gln Asp Ser Pro Ala Leu Ala Ser Val Ala Thr His
 260 265 270

atc ttt caa gat act cca cat cta cag gtc ctt ctg ttc cag aag taa 864
 Ile Phe Gln Asp Thr Pro His Leu Gln Val Leu Leu Phe Gln Lys *
 275 280 285

<210> 110

<211> 287

<212> PRT

<213> Homo sapiens

<400> 110

Met Arg Gln Thr Leu Pro Leu Leu Leu Leu Thr Val Leu Arg Pro Ser
 1 5 10 15
 Trp Ala Asp Pro Pro Gln Glu Lys Val Pro Leu Phe Arg Val Thr Gln
 20 25 30
 Gln Gly Pro Trp Gly Ser Ser Gly Ser Asn Ala Thr Asp Ser Pro Cys
 35 40 45
 Glu Gly Leu Pro Ala Ala Asp Ala Thr Ala Leu Thr Leu Ala Asn Arg
 50 55 60
 Asn Leu Glu Arg Leu Pro Gly Cys Leu Pro Arg Thr Leu Arg Ser Leu
 65 70 75 80
 Asp Ala Ser His Asn Leu Leu Arg Ala Leu Ser Thr Ser Glu Leu Gly
 85 90 95
 His Leu Glu Gln Leu Gln Val Leu Thr Leu Arg His Asn Arg Ile Ala
 100 105 110
 Ala Leu Arg Trp Gly Pro Gly Gly Pro Ala Gly Leu His Thr Leu Asp


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      115              120              125
Leu Ser Tyr Asn Gln Leu Ala Ala Leu Pro Pro Cys Thr Gly Pro Ala
  130              135              140
Leu Ser Ser Leu Arg Ala Leu Ala Leu Ala Gly Asn Pro Leu Arg Ala
  145              150              155              160
Leu Gln Pro Arg Ala Phe Ala Cys Phe Pro Ala Leu Gln Leu Leu Asn
              165              170              175
Leu Ser Cys Thr Ala Leu Gly Arg Gly Ala Gln Gly Gly Ile Ala Glu
              180              185              190
Ala Ala Phe Ala Gly Glu Asp Gly Ala Pro Leu Val Thr Leu Glu Val
  195              200              205
Leu Asp Leu Ser Gly Thr Phe Leu Glu Arg Val Glu Ser Gly Trp Ile
  210              215              220
Arg Asp Leu Pro Lys Leu Thr Ser Leu Tyr Leu Arg Lys Met Pro Arg
  225              230              235              240
Leu Thr Thr Leu Glu Gly Asp Ile Phe Lys Met Thr Pro Asn Leu Gln
              245              250              255
Gln Leu Asp Cys Gln Asp Ser Pro Ala Leu Ala Ser Val Ala Thr His
              260              265              270
Ile Phe Gln Asp Thr Pro His Leu Gln Val Leu Leu Phe Gln Lys
              275              280              285

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<210> 111
<211> 603
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (1)...(603)

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<400> 111

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atg gaa aag gaa tta atc ttc tca ccc tgg cga gtt ttc ctg aaa cta      48
Met Glu Lys Glu Leu Ile Phe Ser Pro Trp Arg Val Phe Leu Lys Leu
  1              5              10              15

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ctt atc ctt agc gtc agc gct gta aga ggt gga gcc gct cag tcc cgc      96
Leu Ile Leu Ser Val Ser Ala Val Arg Gly Gly Ala Ala Gln Ser Arg
              20              25              30

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ggg tgg ctg cag aca gaa ggg gta gtg gac agt gtt gac ttg aat tgc      144
Gly Trp Leu Gln Thr Glu Gly Val Val Asp Ser Val Asp Leu Asn Cys
              35              40              45

```

tgt ccc tcg ttc caa gcc ttt cct gtg aat gaa ccc gaa aac act cga	192
Cys Pro Ser Phe Gln Ala Phe Pro Val Asn Glu Pro Glu Asn Thr Arg	
50 55 60	
cag gtc gtg aat aat cgt ttt aat gag tgt gca aag cgt gcg acg gga	240
Gln Val Val Asn Asn Arg Phe Asn Glu Cys Ala Lys Arg Ala Thr Gly	
65 70 75 80	
cac act ttc ggt ccc ccg cca gag ctc cgg tgc ccc cga gtg acc gct	288
His Thr Phe Gly Pro Pro Pro Glu Leu Arg Cys Pro Arg Val Thr Ala	
85 90 95	
ttc tgc gat cgc gtc cgc cgg gac ccc gtc cct ctt tcc cct tca gtc	336
Phe Cys Asp Arg Val Arg Arg Asp Pro Val Pro Leu Ser Pro Ser Val	
100 105 110	
ttc agg gag ggg gag gcg ctc cgc att agc ggg gca gtt cag caa ccc	384
Phe Arg Glu Gly Glu Ala Leu Arg Ile Ser Gly Ala Val Gln Gln Pro	
115 120 125	
cga ccc cac ccg cgt ggc tcc agg ccc agg ggt ccg ttc act tcc ccg	432
Arg Pro His Pro Arg Gly Ser Arg Pro Arg Gly Pro Phe Thr Ser Pro	
130 135 140	
tcc ggt ttg ggg gac gcc aat tcg cct aag aaa acc ctg gca gaa gag	480
Ser Gly Leu Gly Asp Ala Asn Ser Pro Lys Lys Thr Leu Ala Glu Glu	
145 150 155 160	
cgc gga ccc ttc act aca aac ctc acg tca ggg tta cag cca cat tta	528
Arg Gly Pro Phe Thr Thr Asn Leu Thr Ser Gly Leu Gln Pro His Leu	
165 170 175	
gga acc tct tcg gaa aag ctg aga aat cac tgt ttt gca aaa agc ctt	576
Gly Thr Ser Ser Glu Lys Leu Arg Asn His Cys Phe Ala Lys Ser Leu	
180 185 190	
ctg tac tgt gat ggg gct ttg tgg tga	603
Leu Tyr Cys Asp Gly Ala Leu Trp *	
195 200	

<211> 200
 <212> PRT
 <213> Homo sapiens

<400> 112

Met Glu Lys Glu Leu Ile Phe Ser Pro Trp Arg Val Phe Leu Lys Leu
 1 . 5 10 15
 Leu Ile Leu Ser Val Ser Ala Val Arg Gly Gly Ala Ala Gln Ser Arg
 20 25 30
 Gly Trp Leu Gln Thr Glu Gly Val Val Asp Ser Val Asp Leu Asn Cys
 35 40 45
 Cys Pro Ser Phe Gln Ala Phe Pro Val Asn Glu Pro Glu Asn Thr Arg
 50 55 60
 Gln Val Val Asn Asn Arg Phe Asn Glu Cys Ala Lys Arg Ala Thr Gly
 65 70 75 80
 His Thr Phe Gly Pro Pro Glu Leu Arg Cys Pro Arg Val Thr Ala
 85 90 95
 Phe Cys Asp Arg Val Arg Arg Asp Pro Val Pro Leu Ser Pro Ser Val
 100 105 110
 Phe Arg Glu Gly Glu Ala Leu Arg Ile Ser Gly Ala Val Gln Gln Pro
 115 120 125
 Arg Pro His Pro Arg Gly Ser Arg Pro Arg Gly Pro Phe Thr Ser Pro
 130 135 140
 Ser Gly Leu Gly Asp Ala Asn Ser Pro Lys Lys Thr Leu Ala Glu Glu
 145 150 155 160
 Arg Gly Pro Phe Thr Thr Asn Leu Thr Ser Gly Leu Gln Pro His Leu
 165 170 175
 Gly Thr Ser Ser Glu Lys Leu Arg Asn His Cys Phe Ala Lys Ser Leu
 180 185 190
 Leu Tyr Cys Asp Gly Ala Leu Trp
 195 200

<210> 113
 <211> 285
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(285)

<400> 113

atg gct tca gtg gcc tgg gcc gtc ctc aag gtg ctg ctg ctt ctc ccc

Met Ala Ser Val Ala Trp Ala Val Leu Lys Val Leu Leu Leu Leu Pro
 1 5 10 15

act cag act tgg agc ccc gta gga gca gga aat cca ctt agc tat tcg 96
 Thr Gln Thr Trp Ser Pro Val Gly Ala Gly Asn Pro Leu Ser Tyr Ser
 20 25 30

tct aat cct ttt tca agg ttt tta gct tct ttg cga cgg gtt cga aca 144
 Ser Asn Pro Phe Ser Arg Phe Leu Ala Ser Leu Arg Arg Val Arg Thr
 35 40 45

tcc tcc ttt agc tcg gag aag ttt gtt att acc gat cat ctg aaa cct 192
 Ser Ser Phe Ser Ser Glu Lys Phe Val Ile Thr Asp His Leu Lys Pro
 50 55 60

tct tct ctc aac tcg tca aag tca ttc tcc atc cag ctt tgt tcc gtt 240
 Ser Ser Leu Asn Ser Ser Lys Ser Phe Ser Ile Gln Leu Cys Ser Val
 65 70 75 80

gct ggc gag gcg ttg tgt tcc ttt gga gga gaa gag gcg ctc tga 285
 Ala Gly Glu Ala Leu Cys Ser Phe Gly Gly Glu Glu Ala Leu *
 85 90

<210> 114

<211> 94

<212> PRT

<213> Homo sapiens

<400> 114

Met Ala Ser Val Ala Trp Ala Val Leu Lys Val Leu Leu Leu Leu Pro
 1 5 10 15

Thr Gln Thr Trp Ser Pro Val Gly Ala Gly Asn Pro Leu Ser Tyr Ser
 20 25 30

Ser Asn Pro Phe Ser Arg Phe Leu Ala Ser Leu Arg Arg Val Arg Thr
 35 40 45

Ser Ser Phe Ser Ser Glu Lys Phe Val Ile Thr Asp His Leu Lys Pro
 50 55 60

Ser Ser Leu Asn Ser Ser Lys Ser Phe Ser Ile Gln Leu Cys Ser Val
 65 70 75 80

Ala Gly Glu Ala Leu Cys Ser Phe Gly Gly Glu Glu Ala Leu
 85 90

<220>
<221> CDS
<222> (1)...(312)

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<210> 116
<211> 103
<212> PRT
<213> Homo sapiens
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<400> 116

```

Met Ala Leu Leu Pro Thr Val Leu Cys Leu Trp Ala Gln Ala Gln Val
 1          5          10          15
Gly Val Gln Arg His Asn His Ile Phe Trp Asn Glu Lys Glu His Gly
 20          25          30
His Gly Lys Ser Gly Arg Pro Val Pro Ala Thr Leu Arg Met Thr Arg
 35          40          45
Glu Lys Arg Glu Asn Asp Ser Leu Ser Thr Thr Ser Asp Leu Phe Met
 50          55          60
Thr Leu Pro Ser Ala Gly Glu Met His Ser Pro Ala Arg Arg Trp Pro
 65          70          75          80
Thr Ala Ala Gly Gly Phe Ile Lys Gln Asp Ile Tyr Ile Phe Val Leu
 85          90          95
Leu Glu His Pro Gly Ser Ser
 100

```

<210> 117

<211> 423

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(423)

<400> 117

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atg ccg cca ctg ctg gtc ctg ctc ttg ctc ctg ccg cca cca ctt gca      48
Met Pro Pro Leu Leu Val Leu Leu Leu Leu Leu Pro Pro Pro Leu Ala
 1          5          10          15

cct ccc ctc ttc agc cag tgt ggt ggc agc ggc tgc tcc cga cag ccc      96
Pro Pro Leu Phe Ser Gln Cys Gly Gly Ser Gly Cys Ser Arg Gln Pro
 20          25          30

acc att ccc atc agt aat atg gag ggg caa ata tgt gta aag cct tca      144
Thr Ile Pro Ile Ser Asn Met Glu Gly Gln Ile Cys Val Lys Pro Ser
 35          40          45

ggt gcc aaa gct gct cca gaa ccc ctg gaa gaa tta tca aag atg cgg      192
Gly Ala Lys Ala Ala Pro Glu Pro Leu Glu Glu Leu Ser Lys Met Arg
 50          55          60

```

tcc ctc tct tca att cca tgg tat att ttg tcc ttc agt tct gca gag 240
 Ser Leu Ser Ser Ile Pro Trp Tyr Ile Leu Ser Phe Ser Ser Ala Glu
 65 70 75 80

cct gca atc aaa cat gct aaa gca gag aaa tac aat aag aga cct ata 288
 Pro Ala Ile Lys His Ala Lys Ala Glu Lys Tyr Asn Lys Arg Pro Ile
 85 90 95

ctt gac att agc aga gga agt cca gct gtg tac act aat tat gat aaa 336
 Leu Asp Ile Ser Arg Gly Ser Pro Ala Val Tyr Thr Asn Tyr Asp Lys
 100 105 110

cat cca ttc aca atg tct ggg agg aga cta gcc aca gac ctg gaa aga 384
 His Pro Phe Thr Met Ser Gly Arg Arg Leu Ala Thr Asp Leu Glu Arg
 115 120 125

ggt gaa gaa aaa cga cac cat gaa aaa gga gca aag tga 423
 Gly Glu Glu Lys Arg His His Glu Lys Gly Ala Lys *
 130 135 140

<210> 118

<211> 140

<212> PRT

<213> Homo sapiens

<400> 118

Met Pro Pro Leu Leu Val Leu Leu Leu Leu Leu Pro Pro Pro Leu Ala
 1 5 10 15
 Pro Pro Leu Phe Ser Gln Cys Gly Gly Ser Gly Cys Ser Arg Gln Pro
 20 25 30
 Thr Ile Pro Ile Ser Asn Met Glu Gly Gln Ile Cys Val Lys Pro Ser
 35 40 45
 Gly Ala Lys Ala Ala Pro Glu Pro Leu Glu Glu Leu Ser Lys Met Arg
 50 55 60
 Ser Leu Ser Ser Ile Pro Trp Tyr Ile Leu Ser Phe Ser Ser Ala Glu
 65 70 75 80
 Pro Ala Ile Lys His Ala Lys Ala Glu Lys Tyr Asn Lys Arg Pro Ile
 85 90 95
 Leu Asp Ile Ser Arg Gly Ser Pro Ala Val Tyr Thr Asn Tyr Asp Lys
 100 105 110
 His Pro Phe Thr Met Ser Gly Arg Arg Leu Ala Thr Asp Leu Glu Arg
 115 120 125

Gly Glu Glu Lys Arg His His Glu Lys Gly Ala Lys
 130 135 140

<210> 119
 <211> 336
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(336)

<400> 119

atg gga tgc aga ctg ctg acc ctg ctg tgt ttc cta caa cct gct tcc 48
 Met Gly Cys Arg Leu Leu Thr Leu Leu Cys Phe Leu Gln Pro Ala Ser
 1 5 10 15

agc tcc tcg tgg ctc ttt ggc tcc caa tcc aga gct ttc gcg aac acc 96
 Ser Ser Ser Trp Leu Phe Gly Ser Gln Ser Arg Ala Phe Ala Asn Thr
 20 25 30

aga gcc cct gtg cct ctc cct gca gct ggc tgg gag ttc cag ggc att 144
 Arg Ala Pro Val Pro Leu Pro Ala Ala Gly Trp Glu Phe Gln Gly Ile
 35 40 45

aac aca gac agt ctt tgc cca tca gcc agt gac tgt atg gag ctt gga 192
 Asn Thr Asp Ser Leu Cys Pro Ser Ala Ser Asp Cys Met Glu Leu Gly
 50 55 60

tgt gaa tac aca gct cct gca tcc ctc cga ggc atc tcc aca ccg tct 240
 Cys Glu Tyr Thr Ala Pro Ala Ser Leu Arg Gly Ile Ser Thr Pro Ser
 65 70 75 80

ccc aga gaa tgt ctc gta aaa gct gct cct ctt ggg gag gct ctg ggc 288
 Pro Arg Glu Cys Leu Val Lys Ala Ala Pro Leu Gly Glu Ala Leu Gly
 85 90 95

ttt gga gag agc acc tgg aat tcc cca cta gaa aag ccc aaa aac tga 336
 Phe Gly Glu Ser Thr Trp Asn Ser Pro Leu Glu Lys Pro Lys Asn *
 100 105 110

<210> 120

<211> 111
 <212> PRT
 <213> Homo sapiens

<400> 120

Met	Gly	Cys	Arg	Leu	Leu	Thr	Leu	Leu	Cys	Phe	Leu	Gln	Pro	Ala	Ser
1				5					10					15	
Ser	Ser	Ser	Trp	Leu	Phe	Gly	Ser	Gln	Ser	Arg	Ala	Phe	Ala	Asn	Thr
			20					25					30		
Arg	Ala	Pro	Val	Pro	Leu	Pro	Ala	Ala	Gly	Trp	Glu	Phe	Gln	Gly	Ile
	35						40					45			
Asn	Thr	Asp	Ser	Leu	Cys	Pro	Ser	Ala	Ser	Asp	Cys	Met	Glu	Leu	Gly
	50					55					60				
Cys	Glu	Tyr	Thr	Ala	Pro	Ala	Ser	Leu	Arg	Gly	Ile	Ser	Thr	Pro	Ser
65					70					75				80	
Pro	Arg	Glu	Cys	Leu	Val	Lys	Ala	Ala	Pro	Leu	Gly	Glu	Ala	Leu	Gly
			85						90					95	
Phe	Gly	Glu	Ser	Thr	Trp	Asn	Ser	Pro	Leu	Glu	Lys	Pro	Lys	Asn	
			100					105					110		

<210> 121
 <211> 336
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> (1)...(336)

<400> 121

atg	aag	ctc	ctt	ctt	ctg	ctt	ttg	act	gtt	act	ctg	ctc	ctg	gcc	cag	48
Met	Lys	Leu	Leu	Leu	Leu	Leu	Leu	Thr	Val	Thr	Leu	Leu	Leu	Ala	Gln	
1				5					10					15		
gtc	acc	cca	ggt	ctg	cca	gcc	atg	aaa	ctt	ctt	tac	ctg	ttt	ctt	gcc	96
Val	Thr	Pro	Gly	Leu	Pro	Ala	Met	Lys	Leu	Leu	Tyr	Leu	Phe	Leu	Ala	
			20					25					30			
atc	ctt	ctg	gcc	ata	gaa	gaa	cca	gtg	ata	tca	gta	gag	tgt	tgg	atg	144
Ile	Leu	Leu	Ala	Ile	Glu	Glu	Pro	Val	Ile	Ser	Val	Glu	Cys	Trp	Met	
			35				40					45				
gat	gga	cac	tgc	cgg	ttg	ttg	tgc	aaa	gat	ggt	gaa	gac	agc	atc	ata	192

Asp Gly His Cys Arg Leu Leu Cys Lys Asp Gly Glu Asp Ser Ile Ile
 50 55 60

cgc tgc cga aat cgt aaa cgg tgc tgt gtt cct agt cgt tat tta aca 240
 Arg Cys Arg Asn Arg Lys Arg Cys Cys Val Pro Ser Arg Tyr Leu Thr
 65 70 75 80

atc caa cca gta aca att cat gga atc ctt ggc tgg acc act cct cag 288
 Ile Gln Pro Val Thr Ile His Gly Ile Leu Gly Trp Thr Thr Pro Gln
 85 90 95

atg tcc aca aca gct cca aaa atg aag aca aat ata act aat aga tag 336
 Met Ser Thr Thr Ala Pro Lys Met Lys Thr Asn Ile Thr Asn Arg *
 100 105 110

<210> 122

<211> 111

<212> PRT

<213> Homo sapiens

<400> 122

Met Lys Leu Leu Leu Leu Leu Leu Thr Val Thr Leu Leu Leu Ala Gln
 1 5 10 15
 Val Thr Pro Gly Leu Pro Ala Met Lys Leu Leu Tyr Leu Phe Leu Ala
 20 25 30
 Ile Leu Leu Ala Ile Glu Glu Pro Val Ile Ser Val Glu Cys Trp Met
 35 40 45
 Asp Gly His Cys Arg Leu Leu Cys Lys Asp Gly Glu Asp Ser Ile Ile
 50 55 60
 Arg Cys Arg Asn Arg Lys Arg Cys Cys Val Pro Ser Arg Tyr Leu Thr
 65 70 75 80
 Ile Gln Pro Val Thr Ile His Gly Ile Leu Gly Trp Thr Thr Pro Gln
 85 90 95
 Met Ser Thr Thr Ala Pro Lys Met Lys Thr Asn Ile Thr Asn Arg
 100 105 110

<210> 123

<211> 297

<212> DNA

<213> Homo sapiens

<220>

Gly His Ile Arg Pro Leu Gln Ala Pro Ser Gly Pro Thr Asp Arg Thr
 35 40 45
 Leu Asp Gly Arg Ser Gln Asp Val Asn Gly Ile Ser Val Thr Pro Ser
 50 55 60
 Ser Thr Pro Glu Pro Gln Ala Gly Gly Asn Arg Asp Lys Gln Thr Thr
 65 70 75 80
 His Leu Gly Pro Glu Asp Asp Ala Glu Arg Pro Thr Ser Glu Thr Leu
 85 90 95
 Glu Glu

<210> 125
 <211> 630
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(630)

<400> 125
 atg aga tcc ggg agg cac ccc tcg ctg ctg ctg ctt cta gtg ctg ctg 48
 Met Arg Ser Gly Arg His Pro Ser Leu Leu Leu Leu Val Leu Leu
 1 5 10 15
 ctg tgg ctg ctg cag aca ctg ctc act aga tta ggg ccc act cta acc 96
 Leu Trp Leu Leu Gln Thr Leu Leu Thr Arg Leu Gly Pro Thr Leu Thr
 20 25 30
 cag tgt gac ttc atc tta act gta att cag tta aga att aca tct gca 144
 Gln Cys Asp Phe Ile Leu Thr Val Ile Gln Leu Arg Ile Thr Ser Ala
 35 40 45
 aat agc cta ttt cca aat aag gtc ccg ttc aca ggt aaa ccc aac ggg 192
 Asn Ser Leu Phe Pro Asn Lys Val Pro Phe Thr Gly Lys Pro Asn Gly
 50 55 60
 gtc cat gcg cag tcc tat acg atc tta gta ctc ctc atc gcg tcc cga 240
 Val His Ala Gln Ser Tyr Thr Ile Leu Val Leu Leu Ile Ala Ser Arg
 65 70 75 80
 ggt aat gtt tgc agc tgc gta gag tct atc ttt ata ggc cgg ccg atg 288
 Gly Asn Val Cys Ser Cys Val Glu Ser Ile Phe Ile Gly Arg Pro Met

	85	90	95	
gtt gcg ggt gcc cct cgt cgc ggg tgc gcg cac agg gca acc aga att				336
Val Ala Gly Ala Pro Arg Arg Gly Cys Ala His Arg Ala Thr Arg Ile				
	100	105	110	
aaa acc act att att agg cga aac aag acg ctg gag gtg gta ggc ctc				384
Lys Thr Thr Ile Ile Arg Arg Asn Lys Thr Leu Glu Val Val Gly Leu				
	115	120	125	
aaa ctg ttt ctg ctc gtg tcg acg gcg gac tca gtt ccc cgg aat gtt				432
Lys Leu Phe Leu Leu Val Ser Thr Ala Asp Ser Val Pro Arg Asn Val				
	130	135	140	
cgg gct gtg tcg gag gaa gac gcg gag gaa tca tct gca ggc agt ctc				480
Arg Ala Val Ser Glu Glu Asp Ala Glu Glu Ser Ser Ala Gly Ser Leu				
	145	150	155	160
gtc cac gta ttt caa aaa ttt gcg aat ata ccc gtc gtg ggg aaa tac				528
Val His Val Phe Gln Lys Phe Ala Asn Ile Pro Val Val Gly Lys Tyr				
	165	170	175	
ccg tgc tat ttt ggg gag gct ttg ccc aga ctt tct cga ttg gat tac				576
Pro Cys Tyr Phe Gly Glu Ala Leu Pro Arg Leu Ser Arg Leu Asp Tyr				
	180	185	190	
aga atc tac cgt tac tgc tcg gga tgc cag agg ttg cga tgc tgt gga				624
Arg Ile Tyr Arg Tyr Cys Ser Gly Cys Gln Arg Leu Arg Cys Cys Gly				
	195	200	205	
gag tga				630
Glu *				

<210> 126

<211> 209

<212> PRT

<213> Homo sapiens

<400> 126

Met	Arg	Ser	Gly	Arg	His	Pro	Ser	Leu	Leu	Leu	Leu	Val	Leu	Leu
1				5				10				15		

```

<210> 127
<211> 348
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(348)

<400> 127
atg ggg ccc ctt atc tcc ccc ggc act ttc ccc tac atc cgg ctg caa      48
Met Gly Pro Leu Ile Ser Pro Gly Thr Phe Pro Tyr Ile Arg Leu Gln
 1               5               10              15

cta gaa gct ttc gca cta acc ctc gtg gct gcc cca cgc tgg gcc ctg      96
Leu Glu Ala Phe Ala Leu Thr Leu Val Ala Ala Pro Arg Trp Ala Leu

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```
<210> 128
<211> 115
<212> PRT
<213> Homo sapiens
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<400> 128															
Met	Gly	Pro	Leu	Ile	Ser	Pro	Gly	Thr	Phe	Pro	Tyr	Ile	Arg	Leu	Gln
1				5					10					15	
Leu	Glu	Ala	Phe	Ala	Leu	Thr	Leu	Val	Ala	Ala	Pro	Arg	Trp	Ala	Leu
			20					25					30		
Ala	Phe	Val	Asn	Gly	Ser	Phe	Ile	Lys	Leu	Ser	Pro	Asn	Thr	His	Gly
		35					40					45			
Met	Arg	Val	Thr	Ala	Asp	Ser	Phe	Leu	Pro	Val	Thr	Pro	Ala	Met	Cys
	50					55					60				
Thr	Lys	Ser	Ile	Ser	Asp	Pro	Leu	Leu	Thr	Pro	Pro	Asp	Pro	Val	Lys
65					70					75					80

100	105	110	
caa aga gtc ctg cag cag ctc act gaa gaa gct tcc ctg gat gag gca			384
Gln Arg Val Leu Gln Gln Leu Thr Glu Glu Ala Ser Leu Asp Glu Ala			
115	120	125	
agt ggc ttt aac atc cct gca gag cag gct tct cga ccc tgg acg caa			432
Ser Gly Phe Asn Ile Pro Ala Glu Gln Ala Ser Arg Pro Trp Thr Gln			
130	135	140	
ccc cgc ggg gca gag cct gag gcc cag gat gtg gac ccc agg cct gag			480
Pro Arg Gly Ala Glu Pro Glu Ala Gln Asp Val Asp Pro Arg Pro Glu			
145	150	155	160
gct gag gaa gag gag ctc ccc tgg tgc tgc atc tgc aat gag gat gcc			528
Ala Glu Glu Glu Glu Leu Pro Trp Cys Cys Ile Cys Asn Glu Asp Ala			
165	170	175	
acc cta cgc tgc gct ggc tgc gat ggg gac ctc ttc tgt gcc cgc tgc			576
Thr Leu Arg Cys Ala Gly Cys Asp Gly Asp Leu Phe Cys Ala Arg Cys			
180	185	190	
ttc cga gag ggc cat gat gcc ttt gag ctt aaa gag cac cag aca tct			624
Phe Arg Glu Gly His Asp Ala Phe Glu Leu Lys Glu His Gln Thr Ser			
195	200	205	
gcc tac tct cct cca cgt gca ggc caa gag cac tga			660
Ala Tyr Ser Pro Pro Arg Ala Gly Gln Glu His *			
210	215		

<210> 130

<211> 219

<212> PRT

<213> Homo sapiens

<400> 130

Met Gly Ser Leu Ala Ser Glu Glu Arg Tyr Trp Asp Val Ser Ala Leu	
1 5 10 15	
Leu Met Ala Leu Pro Leu Pro Ala Ala Ser Leu Gln Asn Asp Leu Asn	
20 25 30	
Gln Gly Gly Pro Gly Ser Thr Asn Ser Lys Arg Gln Ala Asn Trp Ser	
35 40 45	

Leu Glu Glu Glu Lys Ser Arg Leu Leu Ala Glu Ala Ala Leu Glu Leu
 50 55 60
 Arg Glu Glu Asn Thr Arg Gln Glu Arg Ile Leu Ala Leu Ala Lys Arg
 65 70 75 80
 Leu Ala Met Leu Arg Gly Gln Asp Pro Glu Arg Val Thr Leu Gln Asp
 85 90 95
 Tyr Arg Leu Pro Asp Ser Asp Asp Glu Asp Glu Glu Thr Ala Ile
 100 105 110
 Gln Arg Val Leu Gln Gln Leu Thr Glu Glu Ala Ser Leu Asp Glu Ala
 115 120 125
 Ser Gly Phe Asn Ile Pro Ala Glu Gln Ala Ser Arg Pro Trp Thr Gln
 130 135 140
 Pro Arg Gly Ala Glu Pro Glu Ala Gln Asp Val Asp Pro Arg Pro Glu
 145 150 155 160
 Ala Glu Glu Glu Glu Leu Pro Trp Cys Cys Ile Cys Asn Glu Asp Ala
 165 170 175
 Thr Leu Arg Cys Ala Gly Cys Asp Gly Asp Leu Phe Cys Ala Arg Cys
 180 185 190
 Phe Arg Glu Gly His Asp Ala Phe Glu Leu Lys Glu His Gln Thr Ser
 195 200 205
 Ala Tyr Ser Pro Pro Arg Ala Gly Gln Glu His
 210 215

<210> 131
 <211> 252
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(252)

<400> 131

atg cag tgg ctt gct ctg ctt ctc cca cat gca ggc cta gcc cag gca 48
 Met Gln Trp Leu Ala Leu Leu Leu Pro His Ala Gly Leu Ala Gln Ala
 1 5 10 15

atg ctg ctg ggc agg tca gag acc tcc aca cct gtc ctc ttc gcg tgc 96
 Met Leu Leu Gly Arg Ser Glu Thr Ser Thr Pro Val Leu Phe Ala Cys
 20 25 30

cac atg gac acg ggc ctg cgc agc gtg gcc aac atc tgg ttc caa tgt 144
 His Met Asp Thr Gly Leu Arg Ser Val Ala Asn Ile Trp Phe Gln Cys

35

40

45

gtg gtt ccc atg cca ctg gct gac tac ccc aat gat gac atg gcc cac 192
 Val Val Pro Met Pro Leu Ala Asp Tyr Pro Asn Asp Asp Met Ala His
 50 55 60

gtt gtc ccc acg gag tcg ctg ctg ctc tca gcc acc gtc acg cgg aga 240
 Val Val Pro Thr Glu Ser Leu Leu Leu Ser Ala Thr Val Thr Arg Arg
 65 70 75 80

gac agg tcc tga 252
 Asp Arg Ser *

<210> 132
 <211> 83
 <212> PRT
 <213> Homo sapiens

<400> 132
 Met Gln Trp Leu Ala Leu Leu Leu Pro His Ala Gly Leu Ala Gln Ala
 1 5 10 15
 Met Leu Leu Gly Arg Ser Glu Thr Ser Thr Pro Val Leu Phe Ala Cys
 20 25 30
 His Met Asp Thr Gly Leu Arg Ser Val Ala Asn Ile Trp Phe Gln Cys
 35 40 45
 Val Val Pro Met Pro Leu Ala Asp Tyr Pro Asn Asp Asp Met Ala His
 50 55 60
 Val Val Pro Thr Glu Ser Leu Leu Leu Ser Ala Thr Val Thr Arg Arg
 65 70 75 80
 Asp Arg Ser

<210> 133
 <211> 378
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(378)

<400> 133

atg	gca	aaa	ata	ggc	gag	gag	agc	tta	aat	tgt	act	ccg	agc	gac	gcg	48
Met	Ala	Lys	Ile	Gly	Glu	Glu	Ser	Leu	Asn	Cys	Thr	Pro	Ser	Asp	Ala	
1				5				10						15		

ctc	cag	tac	aag	gga	atg	ttt	ctt	atg	tat	ctc	ctt	cca	gga	gtg	ttt	96
Leu	Gln	Tyr	Lys	Gly	Met	Phe	Leu	Met	Tyr	Leu	Leu	Pro	Gly	Val	Phe	
			20				25						30			

ggg	cag	gtc	agg	tgc	cca	att	cca	ccc	cag	gac	agt	aag	aga	aag	gtg	144
Gly	Gln	Val	Arg	Cys	Pro	Ile	Pro	Pro	Gln	Asp	Ser	Lys	Arg	Lys	Val	
		35				40						45				

cgg	agc	aag	cac	ccg	gct	cgc	aag	atc	agc	cgc	cgg	gat	aca	aga	acc	192
Arg	Ser	Lys	His	Pro	Ala	Arg	Lys	Ile	Ser	Arg	Arg	Asp	Thr	Arg	Thr	
	50					55					60					

cac	cga	ctg	ctg	ctc	aac	cgc	gca	agt	ccc	tgg	cct	ata	agc	cca	cac	240
His	Arg	Leu	Leu	Leu	Asn	Arg	Ala	Ser	Pro	Trp	Pro	Ile	Ser	Pro	His	
65					70					75					80	

gcc	gaa	aca	aac	agg	aag	gcg	gcc	ctg	gca	cag	atc	gct	cac	tac	cca	288
Ala	Glu	Thr	Asn	Arg	Lys	Ala	Ala	Leu	Ala	Gln	Ile	Ala	His	Tyr	Pro	
				85				90						95		

aaa	ccc	ccg	acc	agc	tgg	aac	gcc	gag	gcc	gac	gac	aac	agt	caa	ggc	336
Lys	Pro	Pro	Thr	Ser	Trp	Asn	Ala	Glu	Ala	Asp	Asp	Asn	Ser	Gln	Gly	
			100				105						110			

aca	aga	ata	cga	gac	cag	gcc	gcg	cca	cac	agg	ctg	ttc	tag			378
Thr	Arg	Ile	Arg	Asp	Gln	Ala	Ala	Pro	His	Arg	Leu	Phe	*			
		115				120						125				

<210> 134

<211> 125

<212> PRT

<213> Homo sapiens

<400> 134

Met	Ala	Lys	Ile	Gly	Glu	Glu	Ser	Leu	Asn	Cys	Thr	Pro	Ser	Asp	Ala	
1				5				10						15		
Leu	Gln	Tyr	Lys	Gly	Met	Phe	Leu	Met	Tyr	Leu	Leu	Pro	Gly	Val	Phe	

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<210> 135
<211> 87
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> (1)...(87)
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atg agc tgg cca cac aaa ctg ctg ctg ctg ctg ctt cta ggt ggc tgc 48
Met Ser Trp Pro His Lys Leu Leu Leu Leu Leu Leu Leu Gly Gly Cys
1 5 10 15

ctt gct ggt ata ctt act ccc tac ttc atg aac tca tga 87
Leu Ala Gly Ile Leu Thr Pro Tyr Phe Met Asn Ser *
20 25

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<210> 136
<211> 28
<212> PRT
<213> Homo sapiens
```

Met Ser Trp Pro His Lys Leu Leu Leu Leu Leu Leu Leu Gly Gly Cys
1 5 10 15
Leu Ala Gly Ile Leu Thr Pro Tyr Phe Met Asn Ser
20 25

<210> 137
 <211> 558
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(558)

<400> 137

atg ggg ctt gat gaa cag ctt ttt ggg gca cta gaa gcc tcc tgg ggt	48
Met Gly Leu Asp Glu Gln Leu Phe Gly Ala Leu Glu Ala Ser Trp Gly	
1 5 10 15	
acc tgt cat gcc ctt gaa cgt ttc ttg gag cgt gcc ttt ttc cac cct	96
Thr Cys His Ala Leu Glu Arg Phe Leu Glu Arg Ala Phe Phe His Pro	
20 25 30	
gcc atg aag ccc gaa gtt ctt cta ttg gca acc aaa ttt cca ctg tcc	144
Ala Met Lys Pro Glu Val Leu Leu Ala Thr Lys Phe Pro Leu Ser	
35 40 45	
ctg ggc aaa aga aaa ggg ccc tca tgt gcg ctt aga aga tct ggc gag	192
Leu Gly Lys Arg Lys Gly Pro Ser Cys Ala Leu Arg Arg Ser Gly Glu	
50 55 60	
gac gaa att tat cat gta acc aga aac cta cag aat ttg ctt ttc ata	240
Asp Glu Ile Tyr His Val Thr Arg Asn Leu Gln Asn Leu Leu Phe Ile	
65 70 75 80	
gga aag tca gcc aaa aat atc aac agc cac aat tta tca gac gcc ttc	288
Gly Lys Ser Ala Lys Asn Ile Asn Ser His Asn Leu Ser Asp Ala Phe	
85 90 95	
agg aaa aat gtc aaa gcc agg cat ttg tct gaa gtg acc tat cct gct	336
Arg Lys Asn Val Lys Ala Arg His Leu Ser Glu Val Thr Tyr Pro Ala	
100 105 110	
tca gaa gtc tat cag cca ttt cca ttc ctg ctt ctg aat gga atc aat	384
Ser Glu Val Tyr Gln Pro Phe Pro Phe Leu Leu Leu Asn Gly Ile Asn	
115 120 125	

Met	Gly	Leu	Asp	Glu	Gln	Leu	Phe	Gly	Ala	Leu	Glu	Ala	Ser	Trp	Gly
1				5				10					15		
Thr	Cys	His	Ala	Leu	Glu	Arg	Phe	Leu	Glu	Arg	Ala	Phe	Phe	His	Pro
			20					25					30		
Ala	Met	Lys	Pro	Glu	Val	Leu	Leu	Leu	Ala	Thr	Lys	Phe	Pro	Leu	Ser
		35					40					45			
Leu	Gly	Lys	Arg	Lys	Gly	Pro	Ser	Cys	Ala	Leu	Arg	Arg	Ser	Gly	Glu
	50					55					60				
Asp	Glu	Ile	Tyr	His	Val	Thr	Arg	Asn	Leu	Gln	Asn	Leu	Leu	Phe	Ile
65					70					75					80
Gly	Lys	Ser	Ala	Lys	Asn	Ile	Asn	Ser	His	Asn	Leu	Ser	Asp	Ala	Phe
			85						90					95	
Arg	Lys	Asn	Val	Lys	Ala	Arg	His	Leu	Ser	Glu	Val	Thr	Tyr	Pro	Ala
			100					105					110		
Ser	Glu	Val	Tyr	Gln	Pro	Phe	Pro	Phe	Leu	Leu	Leu	Asn	Gly	Ile	Asn
		115					120					125			
Gln	Lys	His	Phe	Gln	Pro	Pro	Leu	Leu	Val	Thr	Asp	Gln	Asn	Ser	Cys
	130					135					140				
Gly	Leu	Arg	Val	Ala	Leu	Pro	Pro	Pro	Ala	Pro	Thr	Ser	Ser	Arg	Asn
145					150					155					160

Pro Pro Asp Ala Leu Arg Leu Leu Ser Gln Lys His Asn Gln Asn Asn
 165 170 175

Pro Asn Gly Ile Thr Ile Asn Ile Gln
 180 185

<210> 139

<211> 303

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(303)

<400> 139

atg acc aga gca cct ctc ctg cta cta tgt gtt gcc ctg gtg ctg ctt 48
 Met Thr Arg Ala Pro Leu Leu Leu Leu Cys Val Ala Leu Val Leu Leu
 1 5 10 15

ggg cat gtg aat gga gcc aca gta aga aat gag gac aaa tgg aag cca 96
 Gly His Val Asn Gly Ala Thr Val Arg Asn Glu Asp Lys Trp Lys Pro
 20 25 30

ctc aac aac ccc aga aac aga gat ctg ttt ttc aga agg ctt cag gca 144
 Leu Asn Asn Pro Arg Asn Arg Asp Leu Phe Phe Arg Arg Leu Gln Ala
 35 40 45

tat ttt aag ggc aga ggt ctt gat ctt gga aca ttt cca aat cct ttc 192
 Tyr Phe Lys Gly Arg Gly Leu Asp Leu Gly Thr Phe Pro Asn Pro Phe
 50 55 60

ccc acg aat gaa aat cct aga cct ctc tct ttc cag tca gaa ctt act 240
 Pro Thr Asn Glu Asn Pro Arg Pro Leu Ser Phe Gln Ser Glu Leu Thr
 65 70 75 80

gct tct gca tct gca gat tat gaa gag cag aaa aac tcc ttt cac aat 288
 Ala Ser Ala Ser Ala Asp Tyr Glu Glu Gln Lys Asn Ser Phe His Asn
 85 90 95

tat ctc aaa ggc tga 303
 Tyr Leu Lys Gly *
 100

<210> 140
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 140
 Met Thr Arg Ala Pro Leu Leu Leu Leu Cys Val Ala Leu Val Leu Leu
 1 5 10 15
 Gly His Val Asn Gly Ala Thr Val Arg Asn Glu Asp Lys Trp Lys Pro
 20 25 30
 Leu Asn Asn Pro Arg Asn Arg Asp Leu Phe Phe Arg Arg Leu Gln Ala
 35 40 45
 Tyr Phe Lys Gly Arg Gly Leu Asp Leu Gly Thr Phe Pro Asn Pro Phe
 50 55 60
 Pro Thr Asn Glu Asn Pro Arg Pro Leu Ser Phe Gln Ser Glu Leu Thr
 65 70 75 80
 Ala Ser Ala Ser Ala Asp Tyr Glu Glu Gln Lys Asn Ser Phe His Asn
 85 90 95
 Tyr Leu Lys Gly
 100

<210> 141
 <211> 687
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(687)

<400> 141
 atg cgg ccc ctt aag ccc ggc gcc cct ttg ccc gca ctc ttc ctg ctg 48
 Met Arg Pro Leu Lys Pro Gly Ala Pro Leu Pro Ala Leu Phe Leu Leu
 1 5 10 15
 gcg ctg gct ttg tcc ccg cac gga gcc cac ggg agg ccc cgg ggg cgc 96
 Ala Leu Ala Leu Ser Pro His Gly Ala His Gly Arg Pro Arg Gly Arg
 20 25 30
 agg gga gcg cgc gtc acg gat aag gag ccc aag ccg ttg ctt ttc ctc 144
 Arg Gly Ala Arg Val Thr Asp Lys Glu Pro Lys Pro Leu Leu Phe Leu
 35 40 45

ccc gcg gcc ggg gcc ggc cgg act ccc agc ggc tcc cgg agc gca gga	192
Pro Ala Ala Gly Ala Gly Arg Thr Pro Ser Gly Ser Arg Ser Ala Gly	
50 55 60	
gct ggg cga ggc act cgc ttt ggg aag cct gag att agt aca gca gaa	240
Ala Gly Arg Gly Thr Arg Phe Gly Lys Pro Glu Ile Ser Thr Ala Glu	
65 70 75 80	
aac aga gca tct ctg cag att ccc agc tct cgg aaa gag gtc agg gtc	288
Asn Arg Ala Ser Leu Gln Ile Pro Ser Ser Arg Lys Glu Val Arg Val	
85 90 95	
atg aga cat cca cag gca gag aag tcg tgt gaa tac ggg gaa cac gga	336
Met Arg His Pro Gln Ala Glu Lys Ser Cys Glu Tyr Gly Glu His Gly	
100 105 110	
aaa gcc ccg gaa aag gag gtc cga ggg ggc ggc ccg ggc act tgg ggc	384
Lys Ala Pro Glu Lys Glu Val Arg Gly Gly Gly Pro Gly Thr Trp Gly	
115 120 125	
agc gct gga ggg agg agg gca gga cac gca gga aag gaa ggt ggg gac	432
Ser Ala Gly Gly Arg Arg Ala Gly His Ala Gly Lys Glu Gly Gly Asp	
130 135 140	
aga agc gag aag ctc ctc aca cgt ttc tgt tca cac cca gca aga gca	480
Arg Ser Glu Lys Leu Leu Thr Arg Phe Cys Ser His Pro Ala Arg Ala	
145 150 155 160	
gag caa ggt gaa gct gcc ggc gag gct ggg aca gaa ggg ccc ctc tgc	528
Glu Gln Gly Glu Ala Ala Gly Glu Ala Gly Thr Glu Gly Pro Leu Cys	
165 170 175	
ggg gac att tgg tgg cct cca ccg ggc ttg gga aga gga gag ggc cta	576
Gly Asp Ile Trp Trp Pro Pro Pro Gly Leu Gly Arg Gly Glu Gly Leu	
180 185 190	
ggg tgg cct ggg gat gcc tcg cag cta gcg gct ggc cgt ggg acc aca	624
Gly Trp Pro Gly Asp Ala Ser Gln Leu Ala Ala Gly Arg Gly Thr Thr	
195 200 205	
gct cct gat ccc ttc tcc tca ggc ttt atg gct aag aaa gca aac aag	672
Ala Pro Asp Pro Phe Ser Ser Gly Phe Met Ala Lys Lys Ala Asn Lys	

210

215

220

ggc ttc tta gta tga

Gly Phe Leu Val *

225

687

<210> 142

<211> 228

<212> PRT

<213> Homo sapiens

<400> 142

Met Arg Pro Leu Lys Pro Gly Ala Pro Leu Pro Ala Leu Phe Leu Leu
 1 5 10 15
 Ala Leu Ala Leu Ser Pro His Gly Ala His Gly Arg Pro Arg Gly Arg
 20 25 30
 Arg Gly Ala Arg Val Thr Asp Lys Glu Pro Lys Pro Leu Leu Phe Leu
 35 40 45
 Pro Ala Ala Gly Ala Gly Arg Thr Pro Ser Gly Ser Arg Ser Ala Gly
 50 55 60
 Ala Gly Arg Gly Thr Arg Phe Gly Lys Pro Glu Ile Ser Thr Ala Glu
 65 70 75 80
 Asn Arg Ala Ser Leu Gln Ile Pro Ser Ser Arg Lys Glu Val Arg Val
 85 90 95
 Met Arg His Pro Gln Ala Glu Lys Ser Cys Glu Tyr Gly Glu His Gly
 100 105 110
 Lys Ala Pro Glu Lys Glu Val Arg Gly Gly Gly Pro Gly Thr Trp Gly
 115 120 125
 Ser Ala Gly Gly Arg Arg Ala Gly His Ala Gly Lys Glu Gly Gly Asp
 130 135 140
 Arg Ser Glu Lys Leu Leu Thr Arg Phe Cys Ser His Pro Ala Arg Ala
 145 150 155 160
 Glu Gln Gly Glu Ala Ala Gly Glu Ala Gly Thr Glu Gly Pro Leu Cys
 165 170 175
 Gly Asp Ile Trp Trp Pro Pro Pro Gly Leu Gly Arg Gly Glu Gly Leu
 180 185 190
 Gly Trp Pro Gly Asp Ala Ser Gln Leu Ala Ala Gly Arg Gly Thr Thr
 195 200 205
 Ala Pro Asp Pro Phe Ser Ser Gly Phe Met Ala Lys Lys Ala Asn Lys
 210 215 220
 Gly Phe Leu Val
 225

"13330" 446660

<210> 143
 <211> 393
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(393)

<400> 143

atg ggg ttt ctc cat gtt gag gct ggt ctc gta ctc ctg acc tca ggc	48
Met Gly Phe Leu His Val Glu Ala Gly Leu Val Leu Leu Thr Ser Gly	
1 5 10 15	
gtg gtc ccg ctc gca cga ggg agc ggt cgc cca ggg tgc cgg gaa gtc	96
Val Val Pro Leu Ala Arg Gly Ser Gly Arg Pro Gly Cys Arg Glu Val	
20 25 30	
ggg gac cgg cca gcc gcc gac cgg ccg cac ccc tcc ccg ccg agc tcg	144
Gly Asp Arg Pro Ala Ala Asp Arg Pro His Pro Ser Pro Pro Ser Ser	
35 40 45	
cgc gcc cgc ctc gtc agc acc ttt ccc gca gcg cag ccc cac agt ggt	192
Arg Ala Arg Leu Val Ser Thr Phe Pro Ala Ala Gln Pro His Ser Gly	
50 55 60	
cac gag agc cgc ggc ccg aaa aga cgc gaa ggt ggt gac gtg tcc cgt	240
His Glu Ser Arg Gly Pro Lys Arg Arg Glu Gly Gly Asp Val Ser Arg	
65 70 75 80	
gcc cag ggc gct gcg cag gag gca ttg gca act gac gtc ctg cgc gcc	288
Ala Gln Gly Ala Ala Gln Glu Ala Leu Ala Thr Asp Val Leu Arg Ala	
85 90 95	
gcc tgg tgg aag caa agc agc cga gcc ccc cgg aag cgg cgg cgc ggg	336
Ala Trp Trp Lys Gln Ser Ser Arg Ala Pro Arg Lys Arg Arg Arg Gly	
100 105 110	
cga gtg gag aac gtg act tac gtc atc tgg cgg agg cgt ggg ggc ggt	384
Arg Val Glu Asn Val Thr Tyr Val Ile Trp Arg Arg Arg Gly Gly Gly	
115 120 125	

393

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<210> 144
<211> 130
<212> PRT
<213> Homo sapiens
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[illegible]

```
<210> 145
<211> 666
<212> DNA
<213> Homo sapiens
```

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<220>
<221> CDS
<222> (1)...(666)
```

atg gat acc agc acc tgc tct ggt gga agt ggg agg gga gta aag tgg
 Met Asp Thr Ser Thr Cys Ser Gly Gly Ser Gly Arg Gly Val Lys Trp
 1 5 10 15

1. The first step is to identify the problem. In this case, the problem is that the company is not meeting its sales targets.

180	185	190	
gct gag tct gtc ata gag aat gca agg tct gct gtg ggc atg gag agg			624
Ala Glu Ser Val Ile Glu Asn Ala Arg Ser Ala Val Gly Met Glu Arg			
195	200	205	
agc agt ggt agc aca agt gcc ata gat ttg cca tct act taa			666
Ser Ser Gly Ser Thr Ser Ala Ile Asp Leu Pro Ser Thr *			
210	215	220	

<210> 146
 <211> 221
 <212> PRT
 <213> Homo sapiens

<400> 146

Met	Asp	Thr	Ser	Thr	Cys	Ser	Gly	Gly	Ser	Gly	Arg	Gly	Val	Lys	Trp
1				5					10					15	
Thr	Leu	Arg	Glu	Ser	Leu	Val	Leu	Val	Leu	Phe	Ser	Ala	Leu	Val	Phe
			20					25						30	
Ser	Asn	Ala	Gly	Tyr	Ala	Ser	Cys	Glu	Ala	Val	Thr	Gln	Thr	Asp	Ser
		35					40						45		
Arg	Pro	Leu	Val	Ser	Gln	Gly	Val	Ala	Gly	Phe	Ser	Gly	Ser	Gln	Trp
	50					55					60				
Asp	Val	Gly	Ala	Glu	Ala	Asp	Phe	Ser	Ser	Ser	His	Thr	Leu	Gly	Thr
65					70					75					80
His	Val	Glu	Phe	Ala	Ala	Val	Ser	Cys	Phe	Phe	Gln	Arg	Val	Cys	Glu
				85					90					95	
Phe	Phe	Gln	Phe	Ser	Trp	Tyr	Val	Pro	Val	Val	Val	Leu	Gly	Ala	Lys
			100					105					110		
Leu	His	Asn	Leu	Glu	Glu	Lys	Gly	Glu	Glu	Trp	His	Cys	Leu	Leu	Lys
		115					120					125			
Asp	Asp	Trp	Leu	Leu	Leu	Pro	Ser	Leu	Val	Gln	Phe	Met	Asn	Ser	Leu
	130					135					140				
Glu	Phe	Cys	Asn	Ala	Val	Ile	Gln	Val	Ala	His	Pro	Leu	Ile	Arg	Asn
145					150					155					160
Gln	Leu	Val	Asn	Tyr	Ile	Tyr	Asn	Gly	Phe	Leu	Val	Pro	Val	Leu	Ala
			165					170						175	
Pro	Ala	Leu	His	Lys	Trp	Gln	Leu	Gly	Thr	Val	Lys	Met	Phe	Ser	Lys
		180					185					190			
Ala	Glu	Ser	Val	Ile	Glu	Asn	Ala	Arg	Ser	Ala	Val	Gly	Met	Glu	Arg
		195					200					205			

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<210> 147
<211> 438
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(438)
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<400> 147																	
atg	gct	cgg	gca	ggg	ggc	atg	ggg	ctg	ctg	cga	tta	cag	ctg	ctt	ctg	48	
Met	Ala	Arg	Ala	Gly	Gly	Met	Gly	Leu	Leu	Arg	Leu	Gln	Leu	Leu	Leu		
1		5			10				15								
gta	ctg	ccc	aca	cta	gct	tct	gcc	tgt	gtg	ccc	tgc	atc	tac	ctg	gtt	96	
Val	Leu	Pro	Thr	Leu	Ala	Ser	Ala	Cys	Val	Pro	Cys	Ile	Tyr	Leu	Val		
			20		25				30								
ccc	acg	tgg	acg	tcc	cta	tct	gag	aca	cct	ttt	gga	cca	act	ctg	gac	144	
Pro	Thr	Trp	Thr	Ser	Leu	Ser	Glu	Thr	Pro	Phe	Gly	Pro	Thr	Leu	Asp		
		35			40				45								
aga	ccc	tct	cca	aaa	tca	aag	gtg	cgc	tgg	gct	gct	aac	ctg	atc	caa	192	
Arg	Pro	Ser	Pro	Lys	Ser	Lys	Val	Arg	Trp	Ala	Ala	Asn	Leu	Ile	Gln		
50						55			60								
gac	gag	atc	aat	cta	gaa	gga	cct	gct	ggt	gct	gca	acc	cac	gct	tgg	240	
Asp	Glu	Ile	Asn	Leu	Glu	Gly	Pro	Ala	Gly	Ala	Ala	Thr	His	Ala	Trp		
65						70			75				80				
gtc	acc	ttt	gcc	aga	acc	ggg	gtc	att	tgc	ttt	ggg	ggt	cct	cag	gcc	288	
Val	Thr	Phe	Ala	Arg	Thr	Gly	Val	Ile	Cys	Phe	Gly	Gly	Pro	Gln	Ala		
				85						90		95					
agt	gct	cag	aag	gct	gct	tgt	tgt	aga	tgg	agg	aca	gct	cct	cag	gct	336	
Ser	Ala	Gln	Lys	Ala	Ala	Cys	Cys	Arg	Trp	Arg	Thr	Ala	Pro	Gln	Ala		
			100						105		110						
ggg	aaa	tct	ctc	aat	ggg	aac	tgt	gct	cag	aac	aga	aca	gaa	ctt	ccc	384	
Gly	Lys	Ser	Leu	Asn	Gly	Asn	Cys	Ala	Gln	Asn	Arg	Thr	Glu	Leu	Pro		

115 120 125

gga tac tta gat att tgg gtg gta ttg atc tcc gca tca gtg tcc tcg 432
 Gly Tyr Leu Asp Ile Trp Val Val Leu Ile Ser Ala Ser Val Ser Ser
 130 135 140

ggt tga 438
 Gly *
 145

<210> 148
 <211> 145
 <212> PRT
 <213> Homo sapiens

<400> 148

Met Ala Arg Ala Gly Gly Met Gly Leu Leu Arg Leu Gln Leu Leu Leu
 1 5 10 15
 Val Leu Pro Thr Leu Ala Ser Ala Cys Val Pro Cys Ile Tyr Leu Val
 20 25 30
 Pro Thr Trp Thr Ser Leu Ser Glu Thr Pro Phe Gly Pro Thr Leu Asp
 35 40 45
 Arg Pro Ser Pro Lys Ser Lys Val Arg Trp Ala Ala Asn Leu Ile Gln
 50 55 60
 Asp Glu Ile Asn Leu Glu Gly Pro Ala Gly Ala Ala Thr His Ala Trp
 65 70 75 80
 Val Thr Phe Ala Arg Thr Gly Val Ile Cys Phe Gly Gly Pro Gln Ala
 85 90 95
 Ser Ala Gln Lys Ala Ala Cys Cys Arg Trp Arg Thr Ala Pro Gln Ala
 100 105 110
 Gly Lys Ser Leu Asn Gly Asn Cys Ala Gln Asn Arg Thr Glu Leu Pro
 115 120 125
 Gly Tyr Leu Asp Ile Trp Val Val Leu Ile Ser Ala Ser Val Ser Ser
 130 135 140
 Gly
 145

<210> 149
 <211> 411
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> (1)...(411)

<400> 149

atg tgg gtg ctg ctg ctg ctg ctg ttg gag gca ggc ctc ggg gct ctg	48
Met Trp Val Leu Leu Leu Leu Leu Leu Glu Ala Gly Leu Gly Ala Leu	
1 5 10 15	
act ctg gag ggt tgt gaa ttc cag cgg cac ggg gct gtt gtg tgc ctt	96
Thr Leu Glu Gly Cys Glu Phe Gln Arg His Gly Ala Val Val Cys Leu	
20 25 30	
gtt cac ggc cat ctc cct tcc acc cag tgt cta gcc cag tgt ctg tac	144
Val His Gly His Leu Pro Ser Thr Gln Cys Leu Ala Gln Cys Leu Tyr	
35 40 45	
aca gca gat gcg aag cta cgt gac gtt gtc cgt gaa cca gcc ggg ccc	192
Thr Ala Asp Ala Lys Leu Arg Asp Val Val Arg Glu Pro Ala Gly Pro	
50 55 60	
gcg ttg ccc tac tca act atg tcg agg agc ccc ggt cac cag cgg tct	240
Ala Leu Pro Tyr Ser Thr Met Ser Arg Ser Pro Gly His Gln Arg Ser	
65 70 75 80	
gac cca ttt aac aat tct ggc tct acc gat atc cag ttg ctc gcc cgg	288
Asp Pro Phe Asn Asn Ser Gly Ser Thr Asp Ile Gln Leu Leu Ala Arg	
85 90 95	
gtc cac tca ccg aaa atc tct ata tgt aat tct aag cct aaa aag acg	336
Val His Ser Pro Lys Ile Ser Ile Cys Asn Ser Lys Pro Lys Lys Thr	
100 105 110	
ggc acg caa tac cac gac ggc gac ctg ctc acg ttc gtc ccc agc gat	384
Gly Thr Gln Tyr His Asp Gly Asp Leu Leu Thr Phe Val Pro Ser Asp	
115 120 125	
gca ctg ggg gag gca cgt cgg cgg tga	411
Ala Leu Gly Glu Ala Arg Arg *	
130 135	

<210> 150

<400> 150

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<210> 151
<211> 852
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (1)...(852)

<400> 151

atg gtt tcg gcg gca gcc ccc agc ctc ctc atc ctt ctg ttg ctg ctc	48
Met Val Ser Ala Ala Pro Ser Leu Leu Ile Leu Leu Leu Leu	
1 5 10 15	
ctg ggg tct gtg cct gct acc gac gcc cgc tct gtg ccc ctg aag gcc	96
Leu Gly Ser Val Pro Ala Thr Asp Ala Arg Ser Val Pro Leu Lys Ala	
20 25 30	
acg ttc ctg gag gat gtg gcg ggt agt ggg gag gcc gag ggc tcg tcg	144

Thr	Phe	Leu	Glu	Asp	Val	Ala	Gly	Ser	Gly	Glu	Ala	Glu	Gly	Ser	Ser		
		35					40					45					
gcc	tcc	tcc	ccg	agc	ctc	ccg	cca	ccc	tgg	acc	ccg	gcc	ctc	agc	ccc	192	
Ala	Ser	Ser	Pro	Ser	Leu	Pro	Pro	Pro	Trp	Thr	Pro	Ala	Leu	Ser	Pro		
	50					55					60						
aca	tcg	atg	ggg	ccc	cag	ccc	ata	acc	ctg	ggg	ggc	cca	tca	ccc	ccc	240	
Thr	Ser	Met	Gly	Pro	Gln	Pro	Ile	Thr	Leu	Gly	Gly	Pro	Ser	Pro	Pro		
65					70				75						80		
acc	aac	ttc	ctg	gat	ggg	ata	gtg	gac	ttc	ttc	cgc	cag	tac	gtg	atg	288	
Thr	Asn	Phe	Leu	Asp	Gly	Ile	Val	Asp	Phe	Phe	Arg	Gln	Tyr	Val	Met		
				85				90						95			
ctg	att	gct	gtg	gtg	ggc	tcc	ctg	gcc	ttt	ctg	ctg	atg	ttc	atc	gtc	336	
Leu	Ile	Ala	Val	Val	Gly	Ser	Leu	Ala	Phe	Leu	Leu	Met	Phe	Ile	Val		
			100				105						110				
tgt	gcc	gcg	gtc	atc	acc	cgg	cag	aag	cag	aag	gcc	tcg	gcc	tat	tac	384	
Cys	Ala	Ala	Val	Ile	Thr	Arg	Gln	Lys	Gln	Lys	Ala	Ser	Ala	Tyr	Tyr		
	115					120					125						
cca	tcg	tcc	ttc	ccc	aag	aag	aag	tac	gtg	gac	cag	agt	gac	cgg	gcc	432	
Pro	Ser	Ser	Phe	Pro	Lys	Lys	Lys	Tyr	Val	Asp	Gln	Ser	Asp	Arg	Ala		
	130					135					140						
ggg	ggc	ccc	cgg	gcc	ttc	agt	gag	gtc	ccc	gac	aga	gcc	ccc	gac	agc	480	
Gly	Gly	Pro	Arg	Ala	Phe	Ser	Glu	Val	Pro	Asp	Arg	Ala	Pro	Asp	Ser		
145					150					155					160		
agg	ccc	gag	gaa	gcc	ctg	gat	tcc	tcc	cgg	cag	ctc	cag	gcc	gac	atc	528	
Arg	Pro	Glu	Glu	Ala	Leu	Asp	Ser	Ser	Arg	Gln	Leu	Gln	Ala	Asp	Ile		
				165					170					175			
ttg	gcc	gcc	acc	cag	aac	ctc	aag	tcc	ccc	acc	agg	gct	gca	ctg	ggc	576	
Leu	Ala	Ala	Thr	Gln	Asn	Leu	Lys	Ser	Pro	Thr	Arg	Ala	Ala	Leu	Gly		
			180				185						190				
ggt	ggg	gac	gga	gcc	agg	atg	gtg	gag	ggc	agg	ggc	gca	gag	gaa	gag	624	
Gly	Gly	Asp	Gly	Ala	Arg	Met	Val	Glu	Gly	Arg	Gly	Ala	Glu	Glu	Glu		
	195					200						205					

gag aag ggc agc cag gag ggg gac cag gaa gtc cag gga cat ggg gtc 672
 Glu Lys Gly Ser Gln Glu Gly Asp Gln Glu Val Gln Gly His Gly Val
 210 215 220

cca gtg gag aca cca gag gcg cag gag gag ccg tgc tca ggg gtc ctt 720
 Pro Val Glu Thr Pro Glu Ala Gln Glu Glu Pro Cys Ser Gly Val Leu
 225 230 235 240

gag ggg gct gtg gtg gcc ggt gag ggc caa ggg gag ctg gaa ggg tct 768
 Glu Gly Ala Val Val Ala Gly Glu Gly Gln Gly Glu Leu Glu Gly Ser
 245 250 255

ctc ttg tta gcc cag gaa gcc cag gga cca gtg ggt ccc ccc gaa agc 816
 Leu Leu Leu Ala Gln Glu Ala Gln Gly Pro Val Gly Pro Pro Glu Ser
 260 265 270

ccc tgt gct tgc agc agt gtc cac ccc agt gtc taa 852
 Pro Cys Ala Cys Ser Ser Val His Pro Ser Val *
 275 280

<210> 152

<211> 283

<212> PRT

<213> Homo sapiens

<400> 152

Met Val Ser Ala Ala Ala Pro Ser Leu Leu Ile Leu Leu Leu Leu Leu
 1 5 10 15
 Leu Gly Ser Val Pro Ala Thr Asp Ala Arg Ser Val Pro Leu Lys Ala
 20 25 30
 Thr Phe Leu Glu Asp Val Ala Gly Ser Gly Glu Ala Glu Gly Ser Ser
 35 40 45
 Ala Ser Ser Pro Ser Leu Pro Pro Pro Trp Thr Pro Ala Leu Ser Pro
 50 55 60
 Thr Ser Met Gly Pro Gln Pro Ile Thr Leu Gly Gly Pro Ser Pro Pro
 65 70 75 80
 Thr Asn Phe Leu Asp Gly Ile Val Asp Phe Phe Arg Gln Tyr Val Met
 85 90 95
 Leu Ile Ala Val Val Gly Ser Leu Ala Phe Leu Leu Met Phe Ile Val
 100 105 110
 Cys Ala Ala Val Ile Thr Arg Gln Lys Gln Lys Ala Ser Ala Tyr Tyr
 115 120 125

Pro Ser Ser Phe Pro Lys Lys Lys Tyr Val Asp Gln Ser Asp Arg Ala
 130 135 140
 Gly Gly Pro Arg Ala Phe Ser Glu Val Pro Asp Arg Ala Pro Asp Ser
 145 150 155 160
 Arg Pro Glu Glu Ala Leu Asp Ser Ser Arg Gln Leu Gln Ala Asp Ile
 165 170 175
 Leu Ala Ala Thr Gln Asn Leu Lys Ser Pro Thr Arg Ala Ala Leu Gly
 180 185 190
 Gly Gly Asp Gly Ala Arg Met Val Glu Gly Arg Gly Ala Glu Glu Glu
 195 200 205
 Glu Lys Gly Ser Gln Glu Gly Asp Gln Glu Val Gln Gly His Gly Val
 210 215 220
 Pro Val Glu Thr Pro Glu Ala Gln Glu Glu Pro Cys Ser Gly Val Leu
 225 230 235 240
 Glu Gly Ala Val Val Ala Gly Glu Gly Gln Gly Glu Leu Glu Gly Ser
 245 250 255
 Leu Leu Leu Ala Gln Glu Ala Gln Gly Pro Val Gly Pro Pro Glu Ser
 260 265 270
 Pro Cys Ala Cys Ser Ser Val His Pro Ser Val
 275 280

<210> 153
 <211> 696
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(696)

<400> 153

atg ggc gag ggc tcc aaa ggg ccc tgc atg tgc tgt tcc cct gcc tgg	48
Met Gly Glu Gly Ser Lys Gly Pro Cys Met Cys Cys Ser Pro Ala Trp	
1 5 10 15	
atg ccc acc ccc aag ggt cac ctc ctc cag gaa gcc ttc ctt ctt ctc	96
Met Pro Thr Pro Lys Gly His Leu Leu Gln Glu Ala Phe Leu Leu Leu	
20 25 30	
agg ctg agt tgg ctg gtt act gct gtg cct gct ctt gac tgg gga ttc	144
Arg Leu Ser Trp Leu Val Thr Ala Val Pro Ala Leu Asp Trp Gly Phe	
35 40 45	

<400> 155

att tcc tgg tgt cta gaa ctg tga 264
Ile Ser Trp Cys Leu Glu Leu *
85

<400> 156

Met Leu Met Leu Phe Leu Gln Leu Tyr Phe Val Thr Leu Ala Phe Arg
1 5 10 15

Val Leu Tyr Thr Leu Ser Gln Ala Leu Pro Asp Ile His Gln Leu Pro
 20 25 30
 Glu Arg Ser Pro Leu Cys Pro Ser Arg Arg Phe Ser Thr Val Ser Thr
 35 40 45
 Ala Ala Ile Ala Gln Arg Thr Gln Gln Gln Gly Ala Ile Leu Glu Ala
 50 55 60
 Glu Ser Ser Pro Tyr Gln Thr Pro Asn Leu Leu Ala Pro Arg Ser Trp
 65 70 75 80
 Ile Ser Trp Cys Leu Glu Leu
 85

<210> 157
 <211> 258
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(258)

<400> 157

atg ctg act gcc atg ctt tcc ctc ctt ggc ttt ctc cag gca ctc ttc 48
 Met Leu Thr Ala Met Leu Ser Leu Leu Gly Phe Leu Gln Ala Leu Phe
 1 5 10 15

aca cac aga tgt gtc tac agt ggc agg ttt ggg agc ctg aag agc ggc 96
 Thr His Arg Cys Val Tyr Ser Gly Arg Phe Gly Ser Leu Lys Ser Gly
 20 25 30

tgt gcc cgg tac tgc aat gcc act gtg aag aac gtt ggc tcc aca agc 144
 Cys Ala Arg Tyr Cys Asn Ala Thr Val Lys Asn Val Gly Ser Thr Ser
 35 40 45

atg agc ctt cct ctg tct gtt cgc aca gtg tta gag cca gtc cag act 192
 Met Ser Leu Pro Leu Ser Val Arg Thr Val Leu Glu Pro Val Gln Thr
 50 55 60

cct tgg cta cct cca gac gta tgc agt agt tca tca tgc ctg caa gcg 240
 Pro Trp Leu Pro Pro Asp Val Cys Ser Ser Ser Ser Cys Leu Gln Ala
 65 70 75 80

gta acg aaa acg att tga 258
 Val Thr Lys Thr Ile *

<210> 158
<211> 85
<212> PRT
<213> Homo sapiens

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<210> 159
<211> 624
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> (1)...(624)
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<400> 159																
atg	gtc	cgc	tgc	ctg	ggg	cct	gcg	ctg	ctg	ctg	ctg	ctg	tta	ctg	ggg	48
Met	Val	Arg	Cys	Leu	Gly	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Gly	
1			5			10			15							
tcg	gcg	agc	tcg	gtc	gga	ggg	aac	cga	tgt	gtg	gac	gcg	gcc	gaa	gcc	96
Ser	Ala	Ser	Ser	Val	Gly	Gly	Asn	Arg	Cys	Val	Asp	Ala	Ala	Glu	Ala	
20			25			30										
tgc	acg	gcg	gac	gcg	cgg	tgc	cag	cgt	ttg	cgc	tcc	gag	tat	gtg	gcg	144
Cys	Thr	Ala	Asp	Ala	Arg	Cys	Gln	Arg	Leu	Arg	Ser	Glu	Tyr	Val	Ala	
35			40			45										

cag tgc ctg ggc cgg gct gcg cag ggg ggc tgt ccc gcg ccc gct gcc	192
Gln Cys Leu Gly Arg Ala Ala Gln Gly Gly Cys Pro Ala Pro Ala Ala	
50 55 60	
gcc ggg ccc tgc gcc gct tct tcg ccc gcg ggc gcc cgc gct cac cca	240
Ala Gly Pro Cys Ala Ala Ser Ser Pro Ala Gly Ala Arg Ala His Pro	
65 70 75 80	
cgc act gct ctt ctg ccc gtg cgc cgc ccg gct gcg ccg agc gtc gga	288
Arg Thr Ala Leu Leu Pro Val Arg Arg Pro Ala Ala Pro Ser Val Gly	
85 90 95	
gca ccc ttc gtg ccc tcc tgc gcc ttt tcg ggg ccc ggc cgc ccg ccc	336
Ala Pro Phe Val Pro Ser Cys Ala Phe Ser Gly Pro Gly Arg Pro Pro	
100 105 110	
tcc tgc ctt gag ccc tta aac ttc tgc gag cga cgg aac tgc agg atc	384
Ser Cys Leu Glu Pro Leu Asn Phe Cys Glu Arg Arg Asn Cys Arg Ile	
115 120 125	
ccc ggc ggc gcg gcc gct ggc gag gcg ccc agc gcc ccc gac ggc tgc	432
Pro Gly Gly Ala Ala Ala Gly Glu Ala Pro Ser Ala Pro Asp Gly Cys	
130 135 140	
ctg ctg gac cag agg cgc ccg ctg cct gcg ccc tac gcg ggc ctc gtg	480
Leu Leu Asp Gln Arg Arg Pro Leu Pro Ala Pro Tyr Ala Gly Leu Val	
145 150 155 160	
ggt acg cgc ggc cgg gat ccg ggc gag ggc ggg ggt tct cca ggg gat	528
Gly Thr Arg Gly Arg Asp Pro Gly Glu Gly Gly Gly Ser Pro Gly Asp	
165 170 175	
atc tcc gcc ggc acc gcc gtc acc cct aac tac gtg gac aac gtg agc	576
Ile Ser Ala Gly Thr Ala Val Thr Pro Asn Tyr Val Asp Asn Val Ser	
180 185 190	
gcg cgt ggc gcc ctg gtg cga ctg cgg agc cag cgg gaa ccg gcg tga	624
Ala Arg Gly Ala Leu Val Arg Leu Arg Ser Gln Arg Glu Pro Ala *	
195 200 205	

160

<211> 207
<212> PRT
<213> Homo sapiens

<400> 160

Met	Val	Arg	Cys	Leu	Gly	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Leu	Gly
1				5				10					15	
Ser	Ala	Ser	Ser	Val	Gly	Gly	Asn	Arg	Cys	Val	Asp	Ala	Ala	Glu
			20				25					30		Ala
Cys	Thr	Ala	Asp	Ala	Arg	Cys	Gln	Arg	Leu	Arg	Ser	Glu	Tyr	Val
		35					40					45		Ala
Gln	Cys	Leu	Gly	Arg	Ala	Ala	Gln	Gly	Gly	Cys	Pro	Ala	Pro	Ala
	50					55				60				Ala
Ala	Gly	Pro	Cys	Ala	Ala	Ser	Ser	Pro	Ala	Gly	Ala	Arg	Ala	His
65					70				75					80
Arg	Thr	Ala	Leu	Leu	Pro	Val	Arg	Arg	Pro	Ala	Ala	Pro	Ser	Val
			85						90				95	Gly
Ala	Pro	Phe	Val	Pro	Ser	Cys	Ala	Phe	Ser	Gly	Pro	Gly	Arg	Pro
		100					105					110		Pro
Ser	Cys	Leu	Glu	Pro	Leu	Asn	Phe	Cys	Glu	Arg	Arg	Asn	Cys	Arg
	115					120						125		Ile
Pro	Gly	Gly	Ala	Ala	Ala	Gly	Glu	Ala	Pro	Ser	Ala	Pro	Asp	Gly
	130					135					140			Cys
Leu	Leu	Asp	Gln	Arg	Arg	Pro	Leu	Pro	Ala	Pro	Tyr	Ala	Gly	Leu
145					150					155				160
Gly	Thr	Arg	Gly	Arg	Asp	Pro	Gly	Glu	Gly	Gly	Gly	Ser	Pro	Gly
			165						170				175	Asp
Ile	Ser	Ala	Gly	Thr	Ala	Val	Thr	Pro	Asn	Tyr	Val	Asp	Asn	Val
		180						185				190		Ser
Ala	Arg	Gly	Ala	Leu	Val	Arg	Leu	Arg	Ser	Gln	Arg	Glu	Pro	Ala
	195						200					205		

<210> 161
<211> 423
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(423)

<400> 161

atg tcc acc acc aca tgc caa gtg gtg gcg ttc ctc ctg tcc atc ctg

Met	Ser	Thr	Thr	Thr	Cys	Gln	Val	Val	Ala	Phe	Leu	Leu	Ser	Ile	Leu	
1				5					10					15		
ggg	ctg	gcc	ggc	tgc	atc	gcg	gcc	acc	ggg	atg	gac	atg	tgg	agc	acc	96
Gly	Leu	Ala	Gly	Cys	Ile	Ala	Ala	Thr	Gly	Met	Asp	Met	Trp	Ser	Thr	
			20					25					30			
cag	gac	ctg	tac	gac	aac	ccc	gtc	acc	tcc	gtg	ttc	cag	tac	gaa	ggg	144
Gln	Asp	Leu	Tyr	Asp	Asn	Pro	Val	Thr	Ser	Val	Phe	Gln	Tyr	Glu	Gly	
			35				40					45				
ctc	tgg	agg	agc	tgc	gtg	agg	cag	agt	tca	ggc	ttc	acc	gaa	tgc	agg	192
Leu	Trp	Arg	Ser	Cys	Val	Arg	Gln	Ser	Ser	Gly	Phe	Thr	Glu	Cys	Arg	
	50					55					60					
ccc	tat	ttc	acc	atc	ctg	gga	ctt	cca	gtc	tct	tac	tcc	ccc	atc	ctg	240
Pro	Tyr	Phe	Thr	Ile	Leu	Gly	Leu	Pro	Val	Ser	Tyr	Ser	Pro	Ile	Leu	
	65				70				75					80		
ttt	ctt	ctg	tcc	ttt	cag	tat	acc	ttg	gac	ttg	gtc	ctg	gac	atc	cat	288
Phe	Leu	Leu	Ser	Phe	Gln	Tyr	Thr	Leu	Asp	Leu	Val	Leu	Asp	Ile	His	
				85				90						95		
tgc	tcc	tgc	tcc	cct	gaa	ttc	ccc	cct	cca	cca	ccc	caa	ctg	tcc	tct	336
Cys	Ser	Cys	Ser	Pro	Glu	Phe	Pro	Pro	Pro	Pro	Pro	Gln	Leu	Ser	Ser	
			100				105					110				
cac	aaa	tct	tcc	tcc	aaa	cct	cct	caa	gcc	ccc	aaa	ttg	aat	aaa	gat	384
His	Lys	Ser	Ser	Ser	Lys	Pro	Pro	Gln	Ala	Pro	Lys	Leu	Asn	Lys	Asp	
			115				120					125				
tcc	aca	agt	ctc	tgt	acc	aaa	ccc	aga	gca	ttc	tca	tag				423
Ser	Thr	Ser	Leu	Cys	Thr	Lys	Pro	Arg	Ala	Phe	Ser	*				
	130					135					140					

<210> 162

<211> 140

<212> PRT

<213> Homo sapiens

<400> 162

Met Ser Thr Thr Thr Cys Gln Val Val Ala Phe Leu Leu Ser Ile Leu

1 5 10 15
 Gly Leu Ala Gly Cys Ile Ala Ala Thr Gly Met Asp Met Trp Ser Thr
 20 25 30
 Gln Asp Leu Tyr Asp Asn Pro Val Thr Ser Val Phe Gln Tyr Glu Gly
 35 40 45
 Leu Trp Arg Ser Cys Val Arg Gln Ser Ser Gly Phe Thr Glu Cys Arg
 50 55 60
 Pro Tyr Phe Thr Ile Leu Gly Leu Pro Val Ser Tyr Ser Pro Ile Leu
 65 70 75 80
 Phe Leu Leu Ser Phe Gln Tyr Thr Leu Asp Leu Val Leu Asp Ile His
 85 90 95
 Cys Ser Cys Ser Pro Glu Phe Pro Pro Pro Pro Gln Leu Ser Ser
 100 105 110
 His Lys Ser Ser Ser Lys Pro Pro Gln Ala Pro Lys Leu Asn Lys Asp
 115 120 125
 Ser Thr Ser Leu Cys Thr Lys Pro Arg Ala Phe Ser
 130 135 140

<210> 163

<211> 612

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(612)

<400> 163

atg gtc cgg ctc tgc cag gcc ctg ctg ctg tta gtg gcc act gtg gcc 48
 Met Val Arg Leu Cys Gln Ala Leu Leu Leu Leu Val Ala Thr Val Ala
 1 5 10 15

ctt gca tcc aga aga ttc caa gcc tgg ggc tca aca aag gtg gtg agg 96
 Leu Ala Ser Arg Arg Phe Gln Ala Trp Gly Ser Thr Lys Val Val Arg
 20 25 30

aca ttc caa gat atc cct caa aac tac gtc tat gtg cag cag gca ctc 144
 Thr Phe Gln Asp Ile Pro Gln Asn Tyr Val Tyr Val Gln Gln Ala Leu
 35 40 45

tgg ttc gcc atg aag gag tat aac aag gcc agc ttt agt ata aca agt 192
 Trp Phe Ala Met Lys Glu Tyr Asn Lys Ala Ser Phe Ser Ile Thr Ser
 50 55 60

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<210> 164
<211> 203
<212> PRT
<213> Homo sapiens
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<400> 164

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Met Val Arg Leu Cys Gln Ala Leu Leu Leu Leu Val Ala Thr Val Ala
 1          5          10          15
Leu Ala Ser Arg Arg Phe Gln Ala Trp Gly Ser Thr Lys Val Val Arg
          20          25          30
Thr Phe Gln Asp Ile Pro Gln Asn Tyr Val Tyr Val Gln Gln Ala Leu
          35          40          45
Trp Phe Ala Met Lys Glu Tyr Asn Lys Ala Ser Phe Ser Ile Thr Ser
          50          55          60
Ser Ala Leu Gly Leu Ser Ala Ala Ala Glu Phe Val Gln Cys Glu Cys
65          70          75          80
Trp Arg Lys Glu His Leu Ile Pro Ser Gly Leu Glu Pro His Gly Asn
          85          90          95
Glu Arg Ile Pro Val Tyr Leu Ala Pro Gly Leu Val Ala Phe His Arg
          100          105          110
Cys Thr Gln Val Thr Asp Ser Leu Glu Tyr Tyr Ile Glu Val Lys Ile
          115          120          125
Ala Arg Thr Ile Cys Lys Lys Ile Ser Glu Asp Glu Asn Cys Ala Phe
          130          135          140
Gln Glu Asp Pro Lys Met Gln Lys Ser Gln Arg Ser Arg Leu Leu Leu
145          150          155          160
Leu Gln Ala Lys Met Gly Asp Ser Pro Ser Gln Ala Arg Leu Phe Ser
          165          170          175
Asp Gly Asp Cys His Lys Gly Lys Phe Ile Thr Glu Glu Thr Gly Leu
          180          185          190
Ile Lys Lys Ser Leu Thr Leu Leu Val Val Asp
          195          200

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<210> 165

<211> 534

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(534)

<400> 165

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atg ggt att cag aac tca cca gca ctc ctc ctg atg gct gtc att gtg      48
Met Gly Ile Gln Asn Ser Pro Ala Leu Leu Leu Met Ala Val Ile Val
 1          5          10          15

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ttt ggc aca ttt gct gta agt gta gac agt gac ttg tac act gaa ctg      96

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Phe	Gly	Thr	Phe	Ala	Val	Ser	Val	Asp	Ser	Asp	Leu	Tyr	Thr	Glu	Leu		
			20				25						30				
cgc	tgc	gtg	tat	gtg	aag	tca	acc	ttt	gta	ctt	cat	ccc	aga	aac	atc	144	
Arg	Cys	Val	Tyr	Val	Lys	Ser	Thr	Phe	Val	Leu	His	Pro	Arg	Asn	Ile		
			35				40						45				
cac	aat	ttg	gag	ttg	gtc	tca	gca	gga	ccc	cat	tgc	agc	aaa	gac	gaa	192	
His	Asn	Leu	Glu	Leu	Val	Ser	Ala	Gly	Pro	His	Cys	Ser	Lys	Asp	Glu		
			50				55						60				
gta	atg	atg	gag	cag	tgc	cta	agt	tta	ggc	tcc	tcc	aaa	atg	cag	aat	240	
Val	Met	Met	Glu	Gln	Cys	Leu	Ser	Leu	Gly	Ser	Ser	Lys	Met	Gln	Asn		
			65				70						80				
ttg	agt	cat	gag	cct	gcc	atg	cag	agg	gag	gaa	gga	cgt	tat	gca	gga	288	
Leu	Ser	His	Glu	Pro	Ala	Met	Gln	Arg	Glu	Glu	Gly	Arg	Tyr	Ala	Gly		
			85						90						95		
tac	aaa	aga	aga	ggt	cat	gtt	ata	cag	ccc	tgg	ctt	cca	cgg	aca	cta	336	
Tyr	Lys	Arg	Arg	Gly	His	Val	Ile	Gln	Pro	Trp	Leu	Pro	Arg	Thr	Leu		
			100						105						110		
aca	ctg	aat	tca	aat	ttt	gac	act	gat	aat	ctg	ttg	cca	cca	aat	gga	384	
Thr	Leu	Asn	Ser	Asn	Phe	Asp	Thr	Asp	Asn	Leu	Leu	Pro	Pro	Asn	Gly		
			115						120						125		
aaa	cgt	aaa	caa	ggt	att	cta	agt	gtg	att	aga	gaa	tat	gca	aaa	caa	432	
Lys	Arg	Lys	Gln	Gly	Ile	Leu	Ser	Val	Ile	Arg	Glu	Tyr	Ala	Lys	Gln		
			130						135						140		
gga	aca	agt	aga	aca	ttc	ttc	tct	gga	atc	cga	gac	gat	ggc	tgt	act	480	
Gly	Thr	Ser	Arg	Thr	Phe	Phe	Ser	Gly	Ile	Arg	Asp	Asp	Gly	Cys	Thr		
			145						150						155		
ttc	aca	gag	agc	atg	atg	tta	gat	gta	cat	gaa	ata	acg	cta	aac	cga	528	
Phe	Thr	Glu	Ser	Met	Met	Leu	Asp	Val	His	Glu	Ile	Thr	Leu	Asn	Arg		
			165						170						175		
aaa	tga															534	
Lys	*																

48

Met	Leu	Ser	Lys	Thr	Glu	Gln	Val	Gln	Leu	Gly	Met	Ala	Leu	Ala	Leu	
1				5					10					15		
gct	gcc	ttg	agc	aga	ggc	aga	tct	gtc	ctg	gcc	ttc	ctc	ctg	atc	tct	96
Ala	Ala	Leu	Ser	Arg	Gly	Arg	Ser	Val	Leu	Ala	Phe	Leu	Leu	Ile	Ser	
			20					25					30			
ggg	gaa	gat	gca	gaa	ggc	aaa	tgc	tta	gca	ttt	tat	ctg	ttc	tgc	atc	144
Gly	Glu	Asp	Ala	Glu	Gly	Lys	Cys	Leu	Ala	Phe	Tyr	Leu	Phe	Cys	Ile	
		35					40					45				
cca	ccg	gcg	ggc	ata	att	ccc	agc	tta	gtc	ttt	gac	aag	tct	tcc	aag	192
Pro	Pro	Ala	Gly	Ile	Ile	Pro	Ser	Leu	Val	Phe	Asp	Lys	Ser	Ser	Lys	
	50					55					60					
cct	cag	gcc	cca	gag	ccc	atg	acg	cca	gca	cgc	tcc	ttt	tgg	acg	gtt	240
Pro	Gln	Ala	Pro	Glu	Pro	Met	Thr	Pro	Ala	Arg	Ser	Phe	Trp	Thr	Val	
65					70					75					80	
gtt	tat	gtc	gtc	gtt	atc	tat	cag	aac	agc	acc	tat	tac	gat	gga	ggg	288
Val	Tyr	Val	Val	Val	Ile	Tyr	Gln	Asn	Ser	Thr	Tyr	Tyr	Asp	Gly	Gly	
				85					90					95		
ggc	tgc	cat	aac	agc	ctt	aag	gtg	acc	agc	agc	ccc	gcc	att	gcc	atc	336
Gly	Cys	His	Asn	Ser	Leu	Lys	Val	Thr	Ser	Ser	Pro	Ala	Ile	Ala	Ile	
			100					105					110			
gcc	acc	gcc	gcc	gcc	gct	gcc	atg	gtc	tcc	gtg	gac	cct	gag	aac	ctc	384
Ala	Thr	Ala	Ala	Ala	Ala	Ala	Met	Val	Ser	Val	Asp	Pro	Glu	Asn	Leu	
		115					120					125				
cgg	ggc	ccg	tcc	ccc	tcc	agc	gtg	cag	ccg	cgc	cac	ttc	ctg	acc	ttg	432
Arg	Gly	Pro	Ser	Pro	Ser	Ser	Val	Gln	Pro	Arg	His	Phe	Leu	Thr	Leu	
	130					135					140					
gca	ccc	atc	aaa	ata	ccc	ctc	cgg	acg	tcc	ccc	gtc	tca	ggc	atg	cgt	480
Ala	Pro	Ile	Lys	Ile	Pro	Leu	Arg	Thr	Ser	Pro	Val	Ser	Gly	Met	Arg	
145					150					155					160	
gtc	cat	cca	cta	act	gta	acc	tgc	acg	ctt	cgt	gac	cca	gac	atc	ctt	528
Val	His	Pro	Leu	Thr	Val	Thr	Cys	Thr	Leu	Arg	Asp	Pro	Asp	Ile	Leu	
				165					170					175		

170

acg gta gtg cat aca gcc ctc gag acc tac tca aga gag gac aaa aga 528
 Thr Val Val His Thr Ala Leu Glu Thr Tyr Ser Arg Glu Asp Lys Arg
 165 170 175

gag gct cgg gta gag ctt atc tag 552
 Glu Ala Arg Val Glu Leu Ile *
 180

<210> 170
 <211> 183
 <212> PRT
 <213> Homo sapiens

<400> 170
 Met Ala Leu Arg Val Ser Leu Cys Leu Leu Leu Arg Ala Ser Ser Leu
 1 5 10 15
 Ser Cys Ala Ala Pro Gly Asn Pro Met Ala Gly Asn Arg Lys Leu Pro
 20 25 30
 Lys Glu Glu Gly Thr Thr Ser Tyr His Lys Gly Glu Asp Glu Ser Phe
 35 40 45
 Val Asn Thr Ser Thr Glu Lys Lys Met Ser Lys Asp Trp Lys Ser Asp
 50 55 60
 Asp Ser Met Pro Val Cys Ser Ser Gly Lys Gly Met Gly Ile Ser Thr
 65 70 75 80
 Gly Ile Gln Glu Ser His Lys Glu His Leu Arg Asp Gln Gly Thr Arg
 85 90 95
 Asp Phe Ala Leu Leu Pro Lys Val Met Val Thr Val Thr Ile Ser Met
 100 105 110
 Thr Leu Leu Met Leu Ala Thr Leu Leu Glu Thr Ser Leu Thr His Leu
 115 120 125
 Leu His Leu Glu Lys Ile Gln Thr Phe Asp Glu Val Trp His Tyr Gly
 130 135 140
 His Asp Ser Leu Gln Ile Gly Glu Gly Ser Gly Phe Ile Asp Ile Ser
 145 150 155 160
 Thr Val Val His Thr Ala Leu Glu Thr Tyr Ser Arg Glu Asp Lys Arg
 165 170 175
 Glu Ala Arg Val Glu Leu Ile
 180

<210> 171
 <211> 429
 <212> DNA

1032331426660

<400> 171

cgc agg gtc cac agg gcc ccc agc tgc aag ttg ggg gtt ctt taa 429
Arg Arg Val His Arg Ala Pro Ser Cys Lys Leu Gly Val Leu *
130 135 140

<400> 172

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<210> 173
<211> 534
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (1)...(534)

<400> 173

atg	gct	ctc	agc	ctc	tgg	ccc	ctg	ctg	ctg	ctg	ctg	ctg	ctg	ctg	ctg	ctg	48
Met	Ala	Leu	Ser	Leu	Trp	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	
1				5					10					15			
ctg	ctg	tcc	ttt	gca	ggg	gga	tcc	tct	aga	gtc	gac	ctg	cag	gca	gcg		96
Leu	Leu	Ser	Phe	Ala	Gly	Gly	Ser	Ser	Arg	Val	Asp	Leu	Gln	Ala	Ala		
			20					25					30				

agc tcg cag cgg aag tgt gag agg aga gtt tct gtg ccc ttc tcc ccc 144
 Ser Ser Gln Arg Lys Cys Glu Arg Arg Val Ser Val Pro Phe Ser Pro
 35 40 45

gcc aaa aag aaa acc caa agg gca aga aga aat ttg ggc caa aaa tgc 192
 Ala Lys Lys Lys Thr Gln Arg Ala Arg Arg Asn Leu Gly Gln Lys Cys
 50 55 60

cca aaa gct cgt cac ctt ttt aaa aaa tgg ggt ccc cgt cac aaa att 240
 Pro Lys Ala Arg His Leu Phe Lys Lys Trp Gly Pro Arg His Lys Ile
 65 70 75 80

gtg tcc acc ccc aac act tcc tgg ggg ggc caa agg tct ttg gaa aaa 288
 Val Ser Thr Pro Asn Thr Ser Trp Gly Gly Gln Arg Ser Leu Glu Lys
 85 90 95

agc ttt gcc aaa tca ctc tta gct ttg gac cca cgc tgg gcc gtc ttt 336
 Ser Phe Ala Lys Ser Leu Leu Ala Leu Asp Pro Arg Trp Ala Val Phe
 100 105 110

ggg gac ttt acg ggg gtc tcc agt ggg tta acc aag gaa gac aaa ggt 384
 Gly Asp Phe Thr Gly Val Ser Ser Gly Leu Thr Lys Glu Asp Lys Gly
 115 120 125

ttc gaa gat cca tct caa ggc cta ttg gtt ata aag agg ttt aag ggt 432
 Phe Glu Asp Pro Ser Gln Gly Leu Leu Val Ile Lys Arg Phe Lys Gly
 130 135 140

ttt aag ttg ggg cct ttc cga ttc cgg agg gaa ccc gtc atc ccg ata 480
 Phe Lys Leu Gly Pro Phe Arg Phe Arg Arg Glu Pro Val Ile Pro Ile
 145 150 155 160

aag cag ttg gga tac ccc agg ggc tct gct aga agc tca ggc cag ggt 528
 Lys Gln Leu Gly Tyr Pro Arg Gly Ser Ala Arg Ser Ser Gly Gln Gly
 165 170 175

ggt tga 534
 Gly *

174

<211> 177
 <212> PRT
 <213> Homo sapiens

<400> 174

Met Ala Leu Ser Leu Trp Pro Leu Leu Leu Leu Leu Leu Leu Leu
 1 5 10 15
 Leu Leu Ser Phe Ala Gly Gly Ser Ser Arg Val Asp Leu Gln Ala Ala
 20 25 30
 Ser Ser Gln Arg Lys Cys Glu Arg Arg Val Ser Val Pro Phe Ser Pro
 35 40 45
 Ala Lys Lys Lys Thr Gln Arg Ala Arg Arg Asn Leu Gly Gln Lys Cys
 50 55 60
 Pro Lys Ala Arg His Leu Phe Lys Lys Trp Gly Pro Arg His Lys Ile
 65 70 75 80
 Val Ser Thr Pro Asn Thr Ser Trp Gly Gly Gln Arg Ser Leu Glu Lys
 85 90 95
 Ser Phe Ala Lys Ser Leu Leu Ala Leu Asp Pro Arg Trp Ala Val Phe
 100 105 110
 Gly Asp Phe Thr Gly Val Ser Ser Gly Leu Thr Lys Glu Asp Lys Gly
 115 120 125
 Phe Glu Asp Pro Ser Gln Gly Leu Leu Val Ile Lys Arg Phe Lys Gly
 130 135 140
 Phe Lys Leu Gly Pro Phe Arg Phe Arg Arg Glu Pro Val Ile Pro Ile
 145 150 155 160
 Lys Gln Leu Gly Tyr Pro Arg Gly Ser Ala Arg Ser Ser Gly Gln Gly
 165 170 175
 Gly

<210> 175
 <211> 468
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(468)

<400> 175

atg ggt ttg ggc tcg ctg ctt gct ttt tgg ccg gga agc cgg tgc gtc
 Met Gly Leu Gly Ser Leu Leu Ala Phe Trp Pro Gly Ser Arg Cys Val
 1 5 10 15

ccg ttg gtt gtg gtt tgg gcc tac cgc cgg gtg tgg cgg gtg ggt gct	96
Pro Leu Val Val Val Trp Ala Tyr Arg Arg Val Trp Arg Val Gly Ala	
20 25 30	
ggg gtc ccc ggg ggg ggt ggt cta ttt aaa aaa aaa aag ctc ctc	144
Gly Val Pro Gly Gly Gly Gly Leu Phe Lys Lys Lys Lys Lys Leu Leu	
35 40 45	
gtt cgg aag gtt cga tcg gcc tta aag aac gcc tgc atg gtg ggt cta	192
Val Arg Lys Val Arg Ser Ala Leu Lys Asn Ala Cys Met Val Gly Leu	
50 55 60	
caa gtc att aaa tcc cag act gcc agc ggt cac aga agt cag gag aaa	240
Gln Val Ile Lys Ser Gln Thr Ala Ser Gly His Arg Ser Gln Glu Lys	
65 70 75 80	
gac ctg gaa cag att ctt tct cag agt atc aac aag gaa cca atc ctg	288
Asp Leu Glu Gln Ile Leu Ser Gln Ser Ile Asn Lys Glu Pro Ile Leu	
85 90 95	
cat gac tcc ttg ggg tac cga gct cga att cgt aat cat ggc atc ggc	336
His Asp Ser Leu Gly Tyr Arg Ala Arg Ile Arg Asn His Gly Ile Gly	
100 105 110	
gcc cgc gtt gtt ccg ggt ttg gct ggt gtt gtt cgg tct tct cgg tgc	384
Ala Arg Val Val Pro Gly Leu Ala Gly Val Val Arg Ser Ser Arg Cys	
115 120 125	
cgg cgt atg gcg gcc cta gtt tcg cgt cgc ggc acc ggc att ttt gtg	432
Arg Arg Met Ala Ala Leu Val Ser Arg Arg Gly Thr Gly Ile Phe Val	
130 135 140	
ttg tac gaa gcg gag gaa aag aag act gcg tgc tga	468
Leu Tyr Glu Ala Glu Glu Lys Lys Thr Ala Cys *	
145 150 155	

<210> 176

<211> 155

<212> PRT

<213> Homo sapiens

<400> 176

Met Gly Leu Gly Ser Leu Leu Ala Phe Trp Pro Gly Ser Arg Cys Val
 1 5 10 15
 Pro Leu Val Val Val Trp Ala Tyr Arg Arg Val Trp Arg Val Gly Ala
 20 25 30
 Gly Val Pro Gly Gly Gly Gly Leu Phe Lys Lys Lys Lys Lys Leu Leu
 35 40 45
 Val Arg Lys Val Arg Ser Ala Leu Lys Asn Ala Cys Met Val Gly Leu
 50 55 60
 Gln Val Ile Lys Ser Gln Thr Ala Ser Gly His Arg Ser Gln Glu Lys
 65 70 75 80
 Asp Leu Glu Gln Ile Leu Ser Gln Ser Ile Asn Lys Glu Pro Ile Leu
 85 90 95
 His Asp Ser Leu Gly Tyr Arg Ala Arg Ile Arg Asn His Gly Ile Gly
 100 105 110
 Ala Arg Val Val Pro Gly Leu Ala Gly Val Val Arg Ser Ser Arg Cys
 115 120 125
 Arg Arg Met Ala Ala Leu Val Ser Arg Arg Gly Thr Gly Ile Phe Val
 130 135 140
 Leu Tyr Glu Ala Glu Glu Lys Lys Thr Ala Cys
 145 150 155

<210> 177

<211> 288

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(288)

<400> 177

atg att tta tta cac ctt ctg gat ttg gca aag atc aac gct caa agt 48
 Met Ile Leu Leu His Leu Leu Asp Leu Ala Lys Ile Asn Ala Gln Ser
 1 5 10 15
 gcg acg gcc tct tcg aat tgg gat cgc ccc aag cct agg aat ctt atc 96
 Ala Thr Ala Ser Ser Asn Trp Asp Arg Pro Lys Pro Arg Asn Leu Ile
 20 25 30
 cct ccg att tat gcg aac ccg aca atg tac gtg gag cgg gag gtt gct 144
 Pro Pro Ile Tyr Ala Asn Pro Thr Met Tyr Val Glu Arg Glu Val Ala
 35 40 45

atg gtg tgc ttc ctc aga gtg ctg tgg ctt ctc ctc ttg att ctc tct	48
Met Val Cys Phe Leu Arg Val Leu Trp Leu Leu Leu Leu Ile Leu Ser	
1 5 10 15	
tct ctg cta acc cag aaa acc cgc act gct gag aag aaa tat ggc aca	96
Ser Leu Leu Thr Gln Lys Thr Arg Thr Ala Glu Lys Lys Tyr Gly Thr	
20 25 30	
caa cag ttt ctt cct ctg ctc cat gct gga cca agt ggc ttc ata gct	144
Gln Gln Phe Leu Pro Leu Leu His Ala Gly Pro Ser Gly Phe Ile Ala	
35 40 45	
gcc cag cca gag aca tca aca aca gcc atg ggt gcc aca gct agg agc	192
Ala Gln Pro Glu Thr Ser Thr Thr Ala Met Gly Ala Thr Ala Arg Ser	
50 55 60	
ttc tac ctg gaa cat ccg tta gct ttt gag att cta ttt ttt gcc tta	240
Phe Tyr Leu Glu His Pro Leu Ala Phe Glu Ile Leu Phe Phe Ala Leu	
65 70 75 80	
tat gtg agg gac tgc aat gtg gaa gaa agg agg agg gaa aca ccg gcc	288
Tyr Val Arg Asp Cys Asn Val Glu Glu Arg Arg Arg Glu Thr Pro Ala	
85 90 95	
ctg ggc gcc agg tct cct cct cta gag ctc tcc cca gtt gtg acg ctc	336
Leu Gly Ala Arg Ser Pro Pro Leu Glu Leu Ser Pro Val Val Thr Leu	
100 105 110	
tta ttc aag gcg ttc tcc ccc ccg gac aca gac ttg ctt cat cag cgt	384
Leu Phe Lys Ala Phe Ser Pro Pro Asp Thr Asp Leu Leu His Gln Arg	
115 120 125	
aca gtg cag gct aaa cag tga	405
Thr Val Gln Ala Lys Gln *	
130	

<210> 180

<211> 134

<212> PRT

<213> Homo sapiens

<400> 180

Met Val Cys Phe Leu Arg Val Leu Trp Leu Leu Leu Leu Ile Leu Ser
 1 5 10 15
 Ser Leu Leu Thr Gln Lys Thr Arg Thr Ala Glu Lys Lys Tyr Gly Thr
 20 25 30
 Gln Gln Phe Leu Pro Leu Leu His Ala Gly Pro Ser Gly Phe Ile Ala
 35 40 45
 Ala Gln Pro Glu Thr Ser Thr Thr Ala Met Gly Ala Thr Ala Arg Ser
 50 55 60
 Phe Tyr Leu Glu His Pro Leu Ala Phe Glu Ile Leu Phe Phe Ala Leu
 65 70 75 80
 Tyr Val Arg Asp Cys Asn Val Glu Glu Arg Arg Arg Glu Thr Pro Ala
 85 90 95
 Leu Gly Ala Arg Ser Pro Pro Leu Glu Leu Ser Pro Val Val Thr Leu
 100 105 110
 Leu Phe Lys Ala Phe Ser Pro Pro Asp Thr Asp Leu Leu His Gln Arg
 115 120 125
 Thr Val Gln Ala Lys Gln
 130

<210> 181

<211> 366

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(366)

<400> 181

atg gcg acg ccc agg ggc ctg ggg gcc ctg ctc ctg ctc ctc ctg ctc	48
Met Ala Thr Pro Arg Gly Leu Gly Ala Leu Leu Leu Leu Leu Leu Leu	
1 5 10 15	
ccg acc tca ggg cca cag gca ccc agt ctg agc ttg tct ggg ctg gcg	96
Pro Thr Ser Gly Pro Gln Ala Pro Ser Leu Ser Leu Ser Gly Leu Ala	
20 25 30	
ggc agc ccc agc gaa tca cat gag gat gcc tgg ggc ggg ggg aca gag	144
Gly Ser Pro Ser Glu Ser His Glu Asp Ala Trp Gly Gly Gly Thr Glu	
35 40 45	
aac cac tct gaa aca cac tgt gcc aac caa aag gct ccc cgg act gtc	192
Asn His Ser Glu Thr His Cys Ala Asn Gln Lys Ala Pro Arg Thr Val	

50	55	60	
cca gca gtt ctg agg agt gcc tgt ccc cgt ttt aca gac aag gag atg			240
Pro Ala Val Leu Arg Ser Ala Cys Pro Arg Phe Thr Asp Lys Glu Met			
65	70	75	80
gag ggt gac cga aaa caa ctc aaa gca atc cac caa gcc tct agt cag			288
Glu Gly Asp Arg Lys Gln Leu Lys Ala Ile His Gln Ala Ser Ser Gln			
85	90	95	
cag ctg ctg tgt gtc aac tac cca gag gaa aca ggt gaa aac caa atg			336
Gln Leu Leu Cys Val Asn Tyr Pro Glu Glu Thr Gly Glu Asn Gln Met			
100	105	110	
tca aga ctg ggg gca gag gcc gtg gcc tag			366
Ser Arg Leu Gly Ala Glu Ala Val Ala *			
115	120		

<210> 182

<211> 121

<212> PRT

<213> Homo sapiens

<400> 182

Met Ala Thr Pro Arg Gly Leu Gly Ala Leu Leu Leu Leu Leu Leu Leu			
1	5	10	15
Pro Thr Ser Gly Pro Gln Ala Pro Ser Leu Ser Leu Ser Gly Leu Ala			
20	25	30	
Gly Ser Pro Ser Glu Ser His Glu Asp Ala Trp Gly Gly Gly Thr Glu			
35	40	45	
Asn His Ser Glu Thr His Cys Ala Asn Gln Lys Ala Pro Arg Thr Val			
50	55	60	
Pro Ala Val Leu Arg Ser Ala Cys Pro Arg Phe Thr Asp Lys Glu Met			
65	70	75	80
Glu Gly Asp Arg Lys Gln Leu Lys Ala Ile His Gln Ala Ser Ser Gln			
85	90	95	
Gln Leu Leu Cys Val Asn Tyr Pro Glu Glu Thr Gly Glu Asn Gln Met			
100	105	110	
Ser Arg Leu Gly Ala Glu Ala Val Ala			
115	120		

<210> 183

<211> 693
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(693)

<400> 183

atg	gat	gat	tgt	gaa	gta	aat	gac	tta	cat	gaa	ggg	gca	gga	gtg	aaa	48
Met	Asp	Asp	Cys	Glu	Val	Asn	Asp	Leu	His	Glu	Gly	Ala	Gly	Val	Lys	
1				5				10						15		

cgg	tcc	ttc	ctg	atc	acc	ttg	gtg	tct	cct	ggg	gca	tta	gga	gcc	agg	96
Arg	Ser	Phe	Leu	Ile	Thr	Leu	Val	Ser	Pro	Gly	Ala	Leu	Gly	Ala	Arg	
			20					25					30			

tgt	gat	gta	aga	gaa	gga	gag	aga	ggg	ctt	gtg	aag	act	gag	cga	ggc	144
Cys	Asp	Val	Arg	Glu	Gly	Glu	Arg	Gly	Leu	Val	Lys	Thr	Glu	Arg	Gly	
		35					40				45					

ttg	gtg	aag	caa	ctc	gac	aag	aga	aac	gac	ctg	tgc	aaa	ggg	tgg	acc	192
Leu	Val	Lys	Gln	Leu	Asp	Lys	Arg	Asn	Asp	Leu	Cys	Lys	Gly	Trp	Thr	
	50					55					60					

aca	gcc	cac	aca	ggg	gtg	tgc	aaa	cac	acc	gct	cag	cct	gtc	agg	cat	240
Thr	Ala	His	Thr	Gly	Val	Cys	Lys	His	Thr	Ala	Gln	Pro	Val	Arg	His	
65				70				75						80		

att	tcc	tca	gag	acc	ctg	gca	cgg	cca	ggc	cct	cct	cac	ccc	aac	aat	288
Ile	Ser	Ser	Glu	Thr	Leu	Ala	Arg	Pro	Gly	Pro	Pro	His	Pro	Asn	Asn	
			85					90						95		

aca	gag	gag	tgg	ggg	ctg	gat	gca	ctt	agg	caa	gac	cta	aac	cac	agc	336
Thr	Glu	Glu	Trp	Gly	Leu	Asp	Ala	Leu	Arg	Gln	Asp	Leu	Asn	His	Ser	
			100					105					110			

agt	aag	aca	gca	gct	act	ccc	tgc	tgc	tac	atc	tgt	gga	caa	gca	ggg	384
Ser	Lys	Thr	Ala	Ala	Thr	Pro	Cys	Cys	Tyr	Ile	Cys	Gly	Gln	Ala	Gly	
		115					120				125					

cat	gaa	aat	gtg	tca	gac	agt	ggg	ggc	agc	tgg	att	cct	gat	tct	gtg	432
His	Glu	Asn	Val	Ser	Asp	Ser	Gly	Gly	Ser	Trp	Ile	Pro	Asp	Ser	Val	

130 135 140

att tta tca tca gct ttg aag tat gag gag gca gct gtg gct gcc ata 480
 Ile Leu Ser Ser Ala Leu Lys Tyr Glu Glu Ala Ala Val Ala Ala Ile
 145 150 155 160

ctg gga cca gga agc cag gtc agg aag ctg ctg ctg gcc ctg gca cag 528
 Leu Gly Pro Gly Ser Gln Val Arg Lys Leu Leu Leu Ala Leu Ala Gln
 165 170 175

gca gag gcc acc tca gca gaa gcc aca tca ctg cta gag agg cag cca 576
 Ala Glu Ala Thr Ser Ala Glu Ala Thr Ser Leu Leu Glu Arg Gln Pro
 180 185 190

gga aca ttc cag ctc ctc ctc act tgc ccc gct ggg gca atg cct gcc 624
 Gly Thr Phe Gln Leu Leu Leu Thr Cys Pro Ala Gly Ala Met Pro Ala
 195 200 205

act cct ctg ggt cgc tcc aga cag ctg gtg gcc aaa aag gct gtc act 672
 Thr Pro Leu Gly Arg Ser Arg Gln Leu Val Ala Lys Lys Ala Val Thr
 210 215 220

cac cat cgt ggt gaa cac tga 693
 His His Arg Gly Glu His *
 225 230

<210> 184
 <211> 230
 <212> PRT
 <213> Homo sapiens

<400> 184

Met Asp Asp Cys Glu Val Asn Asp Leu His Glu Gly Ala Gly Val Lys
 1 5 10 15
 Arg Ser Phe Leu Ile Thr Leu Val Ser Pro Gly Ala Leu Gly Ala Arg
 20 25 30
 Cys Asp Val Arg Glu Gly Glu Arg Gly Leu Val Lys Thr Glu Arg Gly
 35 40 45
 Leu Val Lys Gln Leu Asp Lys Arg Asn Asp Leu Cys Lys Gly Trp Thr
 50 55 60
 Thr Ala His Thr Gly Val Cys Lys His Thr Ala Gln Pro Val Arg His
 65 70 75 80

Ile Ser Ser Glu Thr Leu Ala Arg Pro Gly Pro Pro His Pro Asn Asn
 85 90 95
 Thr Glu Glu Trp Gly Leu Asp Ala Leu Arg Gln Asp Leu Asn His Ser
 100 105 110
 Ser Lys Thr Ala Ala Thr Pro Cys Cys Tyr Ile Cys Gly Gln Ala Gly
 115 120 125
 His Glu Asn Val Ser Asp Ser Gly Gly Ser Trp Ile Pro Asp Ser Val
 130 135 140
 Ile Leu Ser Ser Ala Leu Lys Tyr Glu Glu Ala Ala Val Ala Ala Ile
 145 150 155 160
 Leu Gly Pro Gly Ser Gln Val Arg Lys Leu Leu Ala Leu Ala Gln
 165 170 175
 Ala Glu Ala Thr Ser Ala Glu Ala Thr Ser Leu Leu Glu Arg Gln Pro
 180 185 190
 Gly Thr Phe Gln Leu Leu Leu Thr Cys Pro Ala Gly Ala Met Pro Ala
 195 200 205
 Thr Pro Leu Gly Arg Ser Arg Gln Leu Val Ala Lys Lys Ala Val Thr
 210 215 220
 His His Arg Gly Glu His
 225 230

<210> 185
 <211> 1416
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1416)

<400> 185

atg agg ctt ctc ctg gtg ctg ctg ctt ctg gct gct gtg tgt gct gcc	48
Met Arg Leu Leu Leu Val Leu Leu Leu Leu Ala Ala Val Cys Ala Ala	
1 5 10 15	
ctg gtt ggc cca tat gat gct gac ggt cag aca gca cct gct ggg agc	96
Leu Val Gly Pro Tyr Asp Ala Asp Gly Gln Thr Ala Pro Ala Gly Ser	
20 25 30	
tgg tca ctg ctc cca gga tct aat gag ggt gac ccc ttc att ccc atc	144
Trp Ser Leu Leu Pro Gly Ser Asn Glu Gly Asp Pro Phe Ile Pro Ile	
35 40 45	

aca gga cac ccc tat atg aca ccc cta cag tac acc ccc tat agg aca	720
Thr Gly His Pro Tyr Met Thr Pro Leu Gln Tyr Thr Pro Tyr Arg Thr	
225 230 235 240	
cct gaa cag gac acc ccc tac agg acg ctc cct aca gga cac tcc cta	768
Pro Glu Gln Asp Thr Pro Tyr Arg Thr Leu Pro Thr Gly His Ser Leu	
245 250 255	
caa gac act ctt aca gga aac ctc tac agg aca ctc cct aca ggc tcc	816
Gln Asp Thr Leu Thr Gly Asn Leu Tyr Arg Thr Leu Pro Thr Gly Ser	
260 265 270	
cta cag gaa acc cct aca gga cct gcc tta cag gaa acc cct aca agg	864
Leu Gln Glu Thr Pro Thr Gly Pro Ala Leu Gln Glu Thr Pro Thr Arg	
275 280 285	
cgc tcc tac agg aaa cct cca cag gac act ccc tac aga aaa ccc cct	912
Arg Ser Tyr Arg Lys Pro Pro Gln Asp Thr Pro Tyr Arg Lys Pro Pro	
290 295 300	
aca gga cac tcc cta cag gac acc ccc tac agg aca ctc cct aca gga	960
Thr Gly His Ser Leu Gln Asp Thr Pro Tyr Arg Thr Leu Pro Thr Gly	
305 310 315 320	
cac ccc tac agg aca ccc cta ctg gac acc cct ata gga cac tgt aca	1008
His Pro Tyr Arg Thr Pro Leu Leu Asp Thr Pro Ile Gly His Cys Thr	
325 330 335	
gga cac ccc cta cag gac act ccc tac agg aaa ccc cta caa gac act	1056
Gly His Pro Leu Gln Asp Thr Pro Tyr Arg Lys Pro Leu Gln Asp Thr	
340 345 350	
cct aca gga aac ctc tac agg aca ctc cct aca gga aac ccc cta cgg	1104
Pro Thr Gly Asn Leu Tyr Arg Thr Leu Pro Thr Gly Asn Pro Leu Arg	
355 360 365	
gac act ccc tac agg gca ccc cct aca gga cac ccc tac agg acg atc	1152
Asp Thr Pro Tyr Arg Ala Pro Pro Thr Gly His Pro Tyr Arg Thr Ile	
370 375 380	
cct ata gga cac ctg tac agg ata tcc cct aca gga cac tcc cta cag	1200
Pro Ile Gly His Leu Tyr Arg Ile Ser Pro Thr Gly His Ser Leu Gln	

385	390	395	400	
gac act ctg cag gac gct cct aca aaa cac tcc ctg cag gac acc ccc				1248
Asp Thr Leu Gln Asp Ala Pro Thr Lys His Ser Leu Gln Asp Thr Pro				
	405	410	415	
tac agg aca ccc tta cag gac act ccc tac aag aca ccc cct aca gga				1296
Tyr Arg Thr Pro Leu Gln Asp Thr Pro Tyr Lys Thr Pro Pro Thr Gly				
	420	425	430	
cac cct tac agg aca ccc cta cag gac act ccc tac aag aca tcc cct				1344
His Pro Tyr Arg Thr Pro Leu Gln Asp Thr Pro Tyr Lys Thr Ser Pro				
	435	440	445	
aca gga cac tcg tac agg aca cca cct aca gga cac ccc tac agg aca				1392
Thr Gly His Ser Tyr Arg Thr Pro Pro Thr Gly His Pro Tyr Arg Thr				
	450	455	460	
cca cct aca gga tac ccc cta tag				1416
Pro Pro Thr Gly Tyr Pro Leu *				
465	470			

<210> 186
 <211> 471
 <212> PRT
 <213> Homo sapiens

<400> 186

Met	Arg	Leu	Leu	Leu	Val	Leu	Leu	Leu	Leu	Ala	Ala	Val	Cys	Ala	Ala
1				5				10						15	
Leu	Val	Gly	Pro	Tyr	Asp	Ala	Asp	Gly	Gln	Thr	Ala	Pro	Ala	Gly	Ser
			20					25					30		
Trp	Ser	Leu	Leu	Pro	Gly	Ser	Asn	Glu	Gly	Asp	Pro	Phe	Ile	Pro	Ile
		35					40					45			
Thr	Ala	Arg	Gly	Leu	Arg	Asp	Tyr	Gln	Asp	Pro	Tyr	Gly	Glu	Val	Ala
	50					55					60				
Val	Met	Thr	Pro	Leu	Gln	Asn	Thr	Ser	Tyr	Arg	Thr	Pro	Leu	Gln	Asn
65					70				75					80	
Thr	Ser	Tyr	Arg	Thr	Pro	Leu	Gln	Asp	Thr	Pro	Tyr	Arg	Ala	Ser	Leu
				85				90						95	
Gln	Asn	Thr	Ser	Tyr	Arg	Ile	Leu	Pro	Thr	Gly	Tyr	Ser	Leu	Gln	Asp
			100					105					110		

460

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<210> 187
<211> 525
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> (1)...(525)
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<400> 187

atg aag acg ctg tgg ctc ctt ctg tct ctt gct ctg ttt atc ttt cct 48
Met Lys Thr Leu Trp Leu Leu Leu Ser Leu Ala Leu Phe Ile Phe Pro
1 5 10 15

ttc ttg gcg gtg tgt tct gga agt ggc tgc atc cct gac tct gtg gtg 96
Phe Leu Ala Val Cys Ser Gly Ser Gly Cys Ile Pro Asp Ser Val Val
20 25 30

gag tgt ccg gaa ggg gct gtc tgc ccc aca gct gca gct ccc gag gca 144
Glu Cys Pro Glu Gly Ala Val Cys Pro Thr Ala Ala Ala Pro Glu Ala
35 40 45

ccc gcc cct cca cca tgc tca cag gtc cct ttc atc ccc tcc agc cct 192
Pro Ala Pro Pro Pro Cys Ser Gln Val Pro Phe Ile Pro Ser Ser Pro
50 55 60

agg agt gct cta tcc aaa gaa gtc tgg cca att gga tgc agt aca tct 240
Arg Ser Ala Leu Ser Lys Glu Val Trp Pro Ile Gly Cys Ser Thr Ser
65 70 75 80

ttt ggt atg cag aag gtg aat ctc ata att ggt tct att ttt cca gtg 288
Phe Gly Met Gln Lys Val Asn Leu Ile Ile Gly Ser Ile Phe Pro Val
85 90 95

tct gca ttc ctc ctg aag gat gaa gat aac tgc tgt gtc cct ttc ctg 336
Ser Ala Phe Leu Leu Lys Asp Glu Asp Asn Cys Cys Val Pro Phe Leu
100 105 110

ctc aat gaa act ctg caa atc cta cga agc cct ttt acc aca tgg gga 384
Leu Asn Glu Thr Leu Gln Ile Leu Arg Ser Pro Phe Thr Thr Trp Gly

<220>
<221> CDS
<222> (1)...(432)

atg gcc ccg ccg ctc ctg ctg ctg ctg ctg gcc agt gga gcg gcc gcc	48
Met Ala Pro Pro Leu Leu Leu Leu Leu Leu Ala Ser Gly Ala Ala Ala	
1 5 10 15	
tgc ccg ctg ccc tgc gtc tgc cag aac ctg tcc gag tcg ctc agc acc	96
Cys Pro Leu Pro Cys Val Cys Gln Asn Leu Ser Glu Ser Leu Ser Thr	
20 25 30	
ctc tgt gcc cac cga ggc ctg ctg ttt gtg ccg ccc aac gtg gac cgg	144
Leu Cys Ala His Arg Gly Leu Leu Phe Val Pro Pro Asn Val Asp Arg	
35 40 45	
cgc aca gtg gag ctg cgg ctg gct gac aac ttc atc cag gcc ctg ggg	192
Arg Thr Val Glu Leu Arg Leu Ala Asp Asn Phe Ile Gln Ala Leu Gly	
50 55 60	
ccc cct gac ttc cgc aac atg acg gga ctg gtg gac ctg aca ctg tct	240
Pro Pro Asp Phe Arg Asn Met Thr Gly Leu Val Asp Leu Thr Leu Ser	
65 70 75 80	
cgc aat gcc atc acc cgc att ggg gcc cgc gcc ttt ggg gac ctc gag	288
Arg Asn Ala Ile Thr Arg Ile Gly Ala Arg Ala Phe Gly Asp Leu Glu	
85 90 95	
agc ctg cgt tcc ctc cac ctt gac ggc aac agg ctg gtg gag ctg ggc	336
Ser Leu Arg Ser Leu His Leu Asp Gly Asn Arg Leu Val Glu Leu Gly	
100 105 110	
acc ggg agc ctc cgg ggc ccc gtc aat ctg cag cac ctc atc ctc agc	384
Thr Gly Ser Leu Arg Gly Pro Val Asn Leu Gln His Leu Ile Leu Ser	
115 120 125	

ggc aac cag ctg ggc gca tcg cgc cgg gag cct tcg acg act tcc tag 432
 Gly Asn Gln Leu Gly Ala Ser Arg Arg Glu Pro Ser Thr Thr Ser *
 130 135 140

<210> 190
 <211> 143
 <212> PRT
 <213> Homo sapiens

<400> 190
 Met Ala Pro Pro Leu Leu Leu Leu Leu Ala Ser Gly Ala Ala Ala
 1 5 10 15
 Cys Pro Leu Pro Cys Val Cys Gln Asn Leu Ser Glu Ser Leu Ser Thr
 20 25 30
 Leu Cys Ala His Arg Gly Leu Leu Phe Val Pro Pro Asn Val Asp Arg
 35 40 45
 Arg Thr Val Glu Leu Arg Leu Ala Asp Asn Phe Ile Gln Ala Leu Gly
 50 55 60
 Pro Pro Asp Phe Arg Asn Met Thr Gly Leu Val Asp Leu Thr Leu Ser
 65 70 75 80
 Arg Asn Ala Ile Thr Arg Ile Gly Ala Arg Ala Phe Gly Asp Leu Glu
 85 90 95
 Ser Leu Arg Ser Leu His Leu Asp Gly Asn Arg Leu Val Glu Leu Gly
 100 105 110
 Thr Gly Ser Leu Arg Gly Pro Val Asn Leu Gln His Leu Ile Leu Ser
 115 120 125
 Gly Asn Gln Leu Gly Ala Ser Arg Arg Glu Pro Ser Thr Thr Ser
 130 135 140

<210> 191
 <211> 357
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(357)

<400> 191
 atg ggt gta ggc aca gca tcc gtc cta aag aac tgt ctc ttc ctg ggc 48
 Met Gly Val Gly Thr Ala Ser Val Leu Lys Asn Cys Leu Phe Leu Gly
 1 5 10 15

cct ctg gct tgg gct ctc ctg gtc ccc gga gga ctc cag gcg gga agg 96
 Pro Leu Ala Trp Ala Leu Leu Val Pro Gly Gly Leu Gln Ala Gly Arg
 20 25 30

aca ccg ggg gtc tcc ctg gtt aca cca ggc ata ggg ggg gag gac acc 144
 Thr Pro Gly Val Ser Leu Val Thr Pro Gly Ile Gly Gly Glu Asp Thr
 35 40 45

ctt cgg ggg gaa acc cgt ttt tcg cgc cgg tat ttt ttc ggc gat cat 192
 Leu Arg Gly Glu Thr Arg Phe Ser Arg Arg Tyr Phe Phe Gly Asp His
 50 55 60

cat cga gcc ttg gcc cac tgg gac aaa ctt act agt ttt acg gat ctt 240
 His Arg Ala Leu Ala His Trp Asp Lys Leu Thr Ser Phe Thr Asp Leu
 65 70 75 80

cag acc cgg gta aac ggg aga ctt tgc acg ctt atc agc gcc ctg atg 288
 Gln Thr Arg Val Asn Gly Arg Leu Cys Thr Leu Ile Ser Ala Leu Met
 85 90 95

ttc atg gtt tta cct cat tca aat aaa gtg ata agt aag ttc att cga 336
 Phe Met Val Leu Pro His Ser Asn Lys Val Ile Ser Lys Phe Ile Arg
 100 105 110

gag ggt ttc aag caa aaa taa 357
 Glu Gly Phe Lys Gln Lys *
 115

<210> 192

<211> 118

<212> PRT

<213> Homo sapiens

<400> 192

Met Gly Val Gly Thr Ala Ser Val Leu Lys Asn Cys Leu Phe Leu Gly
 1 5 10 15
 Pro Leu Ala Trp Ala Leu Leu Val Pro Gly Gly Leu Gln Ala Gly Arg
 20 25 30
 Thr Pro Gly Val Ser Leu Val Thr Pro Gly Ile Gly Gly Glu Asp Thr
 35 40 45
 Leu Arg Gly Glu Thr Arg Phe Ser Arg Arg Tyr Phe Phe Gly Asp His

50 55 60
 His Arg Ala Leu Ala His Trp Asp Lys Leu Thr Ser Phe Thr Asp Leu
 65 70 75 80
 Gln Thr Arg Val Asn Gly Arg Leu Cys Thr Leu Ile Ser Ala Leu Met
 85 90 95
 Phe Met Val Leu Pro His Ser Asn Lys Val Ile Ser Lys Phe Ile Arg
 100 105 110
 Glu Gly Phe Lys Gln Lys
 115

<210> 193
 <211> 324
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(324)

<400> 193
 atg gtt ctc aaa gtg ccg acg tcc aaa gtc ctg cta gtc ctg gcc acc 48
 Met Val Leu Lys Val Pro Thr Ser Lys Val Leu Leu Val Leu Ala Thr
 1 5 10 15

 ttg ttc gcc gtg gcg gcg atg atc agc agc tgg atg ccc cag gtg gcg 96
 Leu Phe Ala Val Ala Ala Met Ile Ser Ser Trp Met Pro Gln Val Ala
 20 25 30

 gcc agt ccg ctc gca ccc acg gaa tac gaa cag aga cgc atg atg tgc 144
 Ala Ser Pro Leu Ala Pro Thr Glu Tyr Glu Gln Arg Arg Met Met Cys
 35 40 45

 tcc acc ggc ctc agc gat gtg ata cag aag ata tgc gta agc gga acg 192
 Ser Thr Gly Leu Ser Asp Val Ile Gln Lys Ile Cys Val Ser Gly Thr
 50 55 60

 gtg gcc ctt ggc gat gta ttt ccc aac agt ttc ggg aag cgc agg aag 240
 Val Ala Leu Gly Asp Val Phe Pro Asn Ser Phe Gly Lys Arg Arg Lys
 65 70 75 80

 cgc gac ttg cag aac gta acc gat ttg tgc tgc aag tcg ggt ggc tgc 288
 Arg Asp Leu Gln Asn Val Thr Asp Leu Cys Cys Lys Ser Gly Gly Cys
 85 90 95

	20	25	30	
tcc cag cgc ctg cac ctg ctc ctg gag acg ctc acc ttc ccg gct gtt				144
Ser Gln Arg Leu His Leu Leu Leu Glu Thr Leu Thr Phe Pro Ala Val				
	35	40	45	
gcc cta att ctg caa cgt gtc aaa gga caa atg tca cat gtc atg tct				192
Ala Leu Ile Leu Gln Arg Val Lys Gly Gln Met Ser His Val Met Ser				
	50	55	60	
tcc ctg ccc tgg gac agc cgc ctc tac ctg gca ctc atc tct ggc tcc				240
Ser Leu Pro Trp Asp Ser Arg Leu Tyr Leu Ala Leu Ile Ser Gly Ser				
	65	70	75	80
tcg gcg tgg atc agt tac tac atg atc atg ctg tgg agc att tca ctg				288
Ser Ala Trp Ile Ser Tyr Tyr Met Ile Met Leu Trp Ser Ile Ser Leu				
	85	90	95	
agt ttc ttc tgg gtg cct gga ttt tgt gac cgt ttg gtg gcc ttt aag				336
Ser Phe Phe Trp Val Pro Gly Phe Cys Asp Arg Leu Val Ala Phe Lys				
	100	105	110	
aag aga ctt tat gag agt cag ttt tgc cag tac acc tct gga tat aaa				384
Lys Arg Leu Tyr Glu Ser Gln Phe Cys Gln Tyr Thr Ser Gly Tyr Lys				
	115	120	125	
gaa aat caa aat ata agt ttt gtc aac aag aac tac tta tta tac aac				432
Glu Asn Gln Asn Ile Ser Phe Val Asn Lys Asn Tyr Leu Leu Tyr Asn				
	130	135	140	
tac att ggg gct ttt tgc att ttg gct gtg ctg act tat gga agc agg				480
Tyr Ile Gly Ala Phe Cys Ile Leu Ala Val Leu Thr Tyr Gly Ser Arg				
	145	150	155	160
cat aca ctg ggt gtg tga				498
His Thr Leu Gly Val *				
	165			

<210> 196

<211> 165

<212> PRT

<213> Homo sapiens

T08250 "2226660

<400> 196

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Met Arg Glu Ala Gly Gly Leu Lys Asp Thr Thr Gly Lys Leu Trp Lys
 1          5          10          15
Ser Phe Leu Leu Pro Arg Ala Leu Leu Pro Ser Gly Ala Arg Ala Ala
          20          25          30
Ser Gln Arg Leu His Leu Leu Leu Glu Thr Leu Thr Phe Pro Ala Val
          35          40          45
Ala Leu Ile Leu Gln Arg Val Lys Gly Gln Met Ser His Val Met Ser
 50          55          60
Ser Leu Pro Trp Asp Ser Arg Leu Tyr Leu Ala Leu Ile Ser Gly Ser
65          70          75          80
Ser Ala Trp Ile Ser Tyr Tyr Met Ile Met Leu Trp Ser Ile Ser Leu
          85          90          95
Ser Phe Phe Trp Val Pro Gly Phe Cys Asp Arg Leu Val Ala Phe Lys
          100          105          110
Lys Arg Leu Tyr Glu Ser Gln Phe Cys Gln Tyr Thr Ser Gly Tyr Lys
          115          120          125
Glu Asn Gln Asn Ile Ser Phe Val Asn Lys Asn Tyr Leu Leu Tyr Asn
          130          135          140
Tyr Ile Gly Ala Phe Cys Ile Leu Ala Val Leu Thr Tyr Gly Ser Arg
145          150          155          160
His Thr Leu Gly Val
          165

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<210> 197

<211> 573

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(573)

<400> 197

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atg ctg ggc ctc ctg ggg agc aca gcc ctc gtg gga tgg atc aca ggt      48
Met Leu Gly Leu Leu Gly Ser Thr Ala Leu Val Gly Trp Ile Thr Gly
 1          5          10          15

gct gct gtg gcg gtc ctg ctg ctg ctg ctg ctg ctg gcc acc tgc ctt      96
Ala Ala Val Ala Val Leu Leu Leu Leu Leu Leu Leu Ala Thr Cys Leu
          20          25          30

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<211> 190

<213> Homo sapiens

Met	Leu	Gly	Leu	Leu	Gly	Ser	Thr	Ala	Leu	Val	Gly	Trp	Ile	Thr	Gly
1				5					10					15	
Ala	Ala	Val	Ala	Val	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Ala	Thr	Cys	Leu
			20					25					30		
Phe	His	Gly	Arg	Gln	Asp	Cys	Asp	Val	Glu	Arg	Asn	Arg	Thr	Ala	Ala
		35					40					45			
Gly	Gly	Asn	Arg	Val	Arg	Arg	Ala	Gln	Pro	Trp	Pro	Phe	Arg	Arg	Arg
	50					55					60				
Gly	His	Leu	Gly	Ile	Phe	His	His	His	Arg	His	Pro	Gly	His	Glu	Thr
65					70					75					80
Glu	Gly	Glu	Pro	Pro	Glu	Glu	His	Gly	Ala	Pro	Ala	Ile	Ala	Lys	Ser
				85					90					95	
Leu	Leu	Phe	Trp	Met	Gly	Ala	Lys	Ala	Pro	Arg	Gly	Pro	Lys	Val	Ala
			100					105					110		
Gln	Trp	Ala	Met	Glu	Thr	Ala	Val	Ile	Gly	Val	Val	Val	Val	Leu	Phe
		115					120					125			
Val	Val	Thr	Val	Ala	Ile	Thr	Cys	Val	Leu	Cys	Cys	Phe	Ser	Cys	Asp
	130					135					140				
Ser	Arg	Ala	Gln	Asp	Pro	Gln	Gly	Gly	Pro	Gly	Arg	Ser	Phe	Thr	Val
145					150					155					160
Ala	Thr	Phe	Arg	Gln	Glu	Ala	Ser	Leu	Phe	Thr	Gly	Pro	Val	Arg	His
				165					170					175	
Ala	Gln	Pro	Val	Pro	Ser	Ala	Gln	Asp	Phe	Trp	Thr	Phe	Met		
			180					185					190		

<211> 489

<213> Homo sapiens

<221> CDS

<222> (1) ... (489)

atg gcg ctg cct cca ggc cca gcc gcc ctc cgg cac aca ctg ctg ctc
Met Ala Leu Pro Pro Gly Pro Ala Ala Leu Arg His Thr Leu Leu Leu
1 5 10 15

<213> Homo sapiens

[illegible]

$\langle 211 \rangle$ 1113

<213> Homo sapiens

<221> CDS

 $\langle 222 \rangle \quad (1) \dots (1113)$

atg aga act aaa acc cag caa cta aga ttt agg caa aga aaa cag att 48
Met Arg Thr Lys Thr Gln Gln Leu Arg Phe Arg Gln Arg Lys Gln Ile
1 5 10 15

cca gaa tca gca cag agc ctg ctg ctg ctg ctg ctg ctt ctg tct gct 96
Pro Glu Ser Ala Gln Ser Leu Leu Leu Leu Leu Leu Leu Leu Ser Ala

20	25	30	
gct tct gct gct gga ggc att gct aac aca ctc acc caa gcc tta gct Ala Ser Ala Ala Gly Gly Ile Ala Asn Thr Leu Thr Gln Ala Leu Ala 35 40 45			144
ctt aat aga gac atg ttt gca gct gaa tgc ccc agt gct tgt ggt tta Leu Asn Arg Asp Met Phe Ala Ala Glu Cys Pro Ser Ala Cys Gly Leu 50 55 60			192
agc aaa att gtt aac act gtg cga agt tca tgg cct tct gcc aat gcc Ser Lys Ile Val Asn Thr Val Arg Ser Ser Trp Pro Ser Ala Asn Ala 65 70 75 80			240
att gta cag tcc ctg aga gaa aaa agg aga aag ctc ctt ggg ata ata Ile Val Gln Ser Leu Arg Glu Lys Arg Arg Lys Leu Leu Gly Ile Ile 85 90 95			288
agg cag gtg att ctc aga ccc ctc agt gga gtt tgt ggg tgg cgg cag Arg Gln Val Ile Leu Arg Pro Leu Ser Gly Val Cys Gly Trp Arg Gln 100 105 110			336
cag tgg tgg tta gtg agg aaa gcc cgt ctt cag ggt atg tgc aaa tgc Gln Trp Trp Leu Val Arg Lys Ala Arg Leu Gln Gly Met Cys Lys Cys 115 120 125			384
acc aca gct ttg ctg ctg ggg gag ggt ggg gtt gct att agt ggc agc Thr Thr Ala Leu Leu Leu Gly Glu Gly Gly Val Ala Ile Ser Gly Ser 130 135 140			432
agc tgc cgt cag ttg gct ctt agg ctc tgg gga gca tgt gct ttg ggc Ser Cys Arg Gln Leu Ala Leu Arg Leu Trp Gly Ala Cys Ala Leu Gly 145 150 155 160			480
ctt ggt ggt ggc tat cat ggt gtc agt ggt agc agt ggg gag tgg cag Leu Gly Gly Gly Tyr His Gly Val Ser Gly Ser Ser Gly Glu Trp Gln 165 170 175			528
cag cag gga gag cca gtt ctc agg cgc gcg ctc aaa tgc ctg tgc ttg Gln Gln Gly Glu Pro Val Leu Arg Arg Ala Leu Lys Cys Leu Cys Leu 180 185 190			576
cgt tta gga agc gac gag aat ggg tgg ggt caa cac aat act act gct			624

Arg	Leu	Gly	Ser	Asp	Glu	Asn	Gly	Trp	Gly	Gln	His	Asn	Thr	Thr	Ala	
		195					200					205				
gcc	cgc	tca	agg	ttg	aca	gag	tta	aat	gat	ttg	cag	gga	cca	ggc	act	672
Ala	Arg	Ser	Arg	Leu	Thr	Glu	Leu	Asn	Asp	Leu	Gln	Gly	Pro	Gly	Thr	
	210					215				220						
gtg	ggg	ggt	gta	tgg	ctg	ttt	tct	ctg	gcc	tcg	aaa	acc	att	ttc	tcc	720
Val	Gly	Gly	Val	Trp	Leu	Phe	Ser	Leu	Ala	Ser	Lys	Thr	Ile	Phe	Ser	
225					230				235						240	
aga	gcc	gaa	cta	cgc	tct	aag	cac	cgg	aac	tac	ctt	att	agg	gat	aaa	768
Arg	Ala	Glu	Leu	Arg	Ser	Lys	His	Arg	Asn	Tyr	Leu	Ile	Arg	Asp	Lys	
				245				250					255			
tct	cgg	tct	agg	atc	tcg	cca	gaa	tct	cgt	gaa	cta	gtg	cta	agg	cac	816
Ser	Arg	Ser	Arg	Ile	Ser	Pro	Glu	Ser	Arg	Glu	Leu	Val	Leu	Arg	His	
			260					265					270			
aga	acc	cat	ttt	ggc	aca	gaa	aca	tac	tac	ttg	agg	tcg	aga	att	cta	864
Arg	Thr	His	Phe	Gly	Thr	Glu	Thr	Tyr	Tyr	Leu	Arg	Ser	Arg	Ile	Leu	
		275				280						285				
agg	ggt	aag	ctg	acc	ctc	cat	gtg	ata	ccc	gtt	gcg	gct	gtc	aga	cag	912
Arg	Gly	Lys	Leu	Thr	Leu	His	Val	Ile	Pro	Val	Ala	Ala	Val	Arg	Gln	
	290					295				300						
tat	ctt	acc	aca	agc	gac	ctt	cta	aat	agc	gtt	ttt	cta	tat	gat	gct	960
Tyr	Leu	Thr	Thr	Ser	Asp	Leu	Leu	Asn	Ser	Val	Phe	Leu	Tyr	Asp	Ala	
305					310					315					320	
ggc	ggc	agc	cca	gtg	agg	gaa	gtg	caa	caa	gta	tgg	ttc	tcc	tgc	ttg	1008
Gly	Gly	Ser	Pro	Val	Arg	Glu	Val	Gln	Gln	Val	Trp	Phe	Ser	Cys	Leu	
				325				330						335		
tca	act	gtg	gaa	aca	gcg	acc	ctg	aaa	gtg	gag	gag	cca	cag	ctg	gaa	1056
Ser	Thr	Val	Glu	Thr	Ala	Thr	Leu	Lys	Val	Glu	Glu	Pro	Gln	Leu	Glu	
			340				345						350			
tcg	tgt	ccg	tct	gaa	tac	acg	cac	ctt	tcc	tat	gag	cct	tgt	aaa	gcc	1104
Ser	Cys	Pro	Ser	Glu	Tyr	Thr	His	Leu	Ser	Tyr	Glu	Pro	Cys	Lys	Ala	
		355				360						365				

1113

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<210> 202
<211> 370
<212> PRT
<213> Homo sapiens
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<400> 202

Met	Arg	Thr	Lys	Thr	Gln	Gln	Leu	Arg	Phe	Arg	Gln	Arg	Lys	Gln	Ile
1				5					10					15	
Pro	Glu	Ser	Ala	Gln	Ser	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Ser	Ala
			20					25					30		
Ala	Ser	Ala	Ala	Gly	Gly	Ile	Ala	Asn	Thr	Leu	Thr	Gln	Ala	Leu	Ala
		35					40					45			
Leu	Asn	Arg	Asp	Met	Phe	Ala	Ala	Glu	Cys	Pro	Ser	Ala	Cys	Gly	Leu
	50					55				60					
Ser	Lys	Ile	Val	Asn	Thr	Val	Arg	Ser	Ser	Trp	Pro	Ser	Ala	Asn	Ala
65					70					75					80
Ile	Val	Gln	Ser	Leu	Arg	Glu	Lys	Arg	Arg	Lys	Leu	Leu	Gly	Ile	Ile
				85					90					95	
Arg	Gln	Val	Ile	Leu	Arg	Pro	Leu	Ser	Gly	Val	Cys	Gly	Trp	Arg	Gln
			100					105					110		
Gln	Trp	Trp	Leu	Val	Arg	Lys	Ala	Arg	Leu	Gln	Gly	Met	Cys	Lys	Cys
		115					120					125			
Thr	Thr	Ala	Leu	Leu	Leu	Gly	Glu	Gly	Gly	Val	Ala	Ile	Ser	Gly	Ser
		130				135					140				
Ser	Cys	Arg	Gln	Leu	Ala	Leu	Arg	Leu	Trp	Gly	Ala	Cys	Ala	Leu	Gly
145					150					155					160
Leu	Gly	Gly	Gly	Tyr	His	Gly	Val	Ser	Gly	Ser	Ser	Gly	Glu	Trp	Gln
				165					170					175	
Gln	Gln	Gly	Glu	Pro	Val	Leu	Arg	Arg	Ala	Leu	Lys	Cys	Leu	Cys	Leu
			180					185					190		
Arg	Leu	Gly	Ser	Asp	Glu	Asn	Gly	Trp	Gly	Gln	His	Asn	Thr	Thr	Ala
		195					200					205			
Ala	Arg	Ser	Arg	Leu	Thr	Glu	Leu	Asn	Asp	Leu	Gln	Gly	Pro	Gly	Thr
		210				215					220				
Val	Gly	Gly	Val	Trp	Leu	Phe	Ser	Leu	Ala	Ser	Lys	Thr	Ile	Phe	Ser
225					230					235					240
Arg	Ala	Glu	Leu	Arg	Ser	Lys	His	Arg	Asn	Tyr	Leu	Ile	Arg	Asp	Lys
				245					250					255	

Ser Arg Ser Arg Ile Ser Pro Glu Ser Arg Glu Leu Val Leu Arg His
 260 265 270
 Arg Thr His Phe Gly Thr Glu Thr Tyr Tyr Leu Arg Ser Arg Ile Leu
 275 280 285
 Arg Gly Lys Leu Thr Leu His Val Ile Pro Val Ala Ala Val Arg Gln
 290 295 300
 Tyr Leu Thr Thr Ser Asp Leu Leu Asn Ser Val Phe Leu Tyr Asp Ala
 305 310 315 320
 Gly Gly Ser Pro Val Arg Glu Val Gln Gln Val Trp Phe Ser Cys Leu
 325 330 335
 Ser Thr Val Glu Thr Ala Thr Leu Lys Val Glu Glu Pro Gln Leu Glu
 340 345 350
 Ser Cys Pro Ser Glu Tyr Thr His Leu Ser Tyr Glu Pro Cys Lys Ala
 355 360 365
 Ser Arg
 370

<210> 203
 <211> 279
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(279)

<400> 203

atg gag ttg tgg tgg gag tgg gca ttg ctg gcc act ctc ctg gtg ctt 48
 Met Glu Leu Trp Trp Glu Trp Ala Leu Leu Ala Thr Leu Leu Val Leu
 1 5 10 15

gtt gca ggg agc cag aaa ata tgt cag agt ata gag gac ccc cca tac 96
 Val Ala Gly Ser Gln Lys Ile Cys Gln Ser Ile Glu Asp Pro Pro Tyr
 20 25 30

aat tta aag aat aag gag gag gag gag gag aag gag gag gag gga gag 144
 Asn Leu Lys Asn Lys Glu Glu Glu Glu Glu Lys Glu Glu Glu Gly Glu
 35 40 45

gag aag gta gaa cat aac gtt tcc atc cag gtt aag aaa cag cca ggc 192
 Glu Lys Val Glu His Asn Val Ser Ile Gln Val Lys Lys Gln Pro Gly
 50 55 60

205

ctt ggt ctt ctg ctc ctg gac atc ccg gcc ttc act gac cac cgt ctg 240
 Leu Gly Leu Leu Leu Leu Asp Ile Pro Ala Phe Thr Asp His Arg Leu
 65 70 75 80

aac agg tcc gag ccc tgc tct acc ctg tgc ttt gct tga 279
 Asn Arg Ser Glu Pro Cys Ser Thr Leu Cys Phe Ala *
 85 90

<210> 204
 <211> 92
 <212> PRT
 <213> Homo sapiens

<400> 204
 Met Glu Leu Trp Trp Glu Trp Ala Leu Leu Ala Thr Leu Leu Val Leu
 1 5 10 15
 Val Ala Gly Ser Gln Lys Ile Cys Gln Ser Ile Glu Asp Pro Pro Tyr
 20 25 30
 Asn Leu Lys Asn Lys Glu Glu Glu Glu Lys Glu Glu Glu Gly Glu
 35 40 45
 Glu Lys Val Glu His Asn Val Ser Ile Gln Val Lys Lys Gln Pro Gly
 50 55 60
 Leu Gly Leu Leu Leu Leu Asp Ile Pro Ala Phe Thr Asp His Arg Leu
 65 70 75 80
 Asn Arg Ser Glu Pro Cys Ser Thr Leu Cys Phe Ala
 85 90

<210> 205
 <211> 657
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(657)

<400> 205
 atg cga gac aaa gca gcc cct gcc tgg aca gtg ctg gcc ctg atg caa 48
 Met Arg Asp Lys Ala Ala Pro Ala Trp Thr Val Leu Ala Leu Met Gln
 1 5 10 15

ggg gtg cag gca aag aag gag agg ccc tct tgg ctt cgg gat gca gtt 96

CCDS:CCDS1000.1

Gly	Val	Gln	Ala	Lys	Lys	Glu	Arg	Pro	Ser	Trp	Leu	Arg	Asp	Ala	Val		
		20						25					30				
ctc	tgc	tcc	acc	aca	cca	gtg	ccc	agg	gcc	ttt	ccc	atg	gca	aag	cac	144	
Leu	Cys	Ser	Thr	Thr	Pro	Val	Pro	Arg	Ala	Phe	Pro	Met	Ala	Lys	His		
		35					40				45						
caa	cac	ctg	ccc	tta	ttt	aaa	agc	tta	tct	gta	gcc	cag	cag	aaa	aca	192	
Gln	His	Leu	Pro	Leu	Phe	Lys	Ser	Leu	Ser	Val	Ala	Gln	Gln	Lys	Thr		
	50					55				60							
agg	cac	gac	aca	tat	ttg	agg	ttt	aac	atc	ttg	att	ctc	agg	ctt	tat	240	
Arg	His	Asp	Thr	Tyr	Leu	Arg	Phe	Asn	Ile	Leu	Ile	Leu	Arg	Leu	Tyr		
65					70					75					80		
aac	act	gga	tat	tat	tgg	caa	cac	cat	gaa	aca	aag	aaa	cag	aag	ctt	288	
Asn	Thr	Gly	Tyr	Tyr	Trp	Gln	His	His	Glu	Thr	Lys	Lys	Gln	Lys	Leu		
				85					90				95				
ctg	ccc	act	cct	cca	cat	gtg	aca	tta	gga	att	cag	tgt	agg	aca	gtg	336	
Leu	Pro	Thr	Pro	Pro	His	Val	Thr	Leu	Gly	Ile	Gln	Cys	Arg	Thr	Val		
			100					105					110				
aag	gac	aaa	tca	cta	cac	ctg	agt	tct	gct	atc	ttg	gtt	ctt	tct	gtg	384	
Lys	Asp	Lys	Ser	Leu	His	Leu	Ser	Ser	Ala	Ile	Leu	Val	Leu	Ser	Val		
		115					120					125					
acc	aaa	cag	tct	gta	cgc	ccc	ctg	cag	agg	aac	cag	cat	ctg	gct	gac	432	
Thr	Lys	Gln	Ser	Val	Arg	Pro	Leu	Gln	Arg	Asn	Gln	His	Leu	Ala	Asp		
	130					135					140						
atc	tcc	aca	ggc	gca	gca	acc	acc	tgc	tgg	cca	gaa	gag	gta	aca	tta	480	
Ile	Ser	Thr	Gly	Ala	Ala	Thr	Thr	Cys	Trp	Pro	Glu	Glu	Val	Thr	Leu		
145					150					155					160		
gta	gca	tat	tca	gtt	cac	acc	gaa	cgt	cat	tat	gaa	aat	cag	cag	aac	528	
Val	Ala	Tyr	Ser	Val	His	Thr	Glu	Arg	His	Tyr	Glu	Asn	Gln	Gln	Asn		
				165					170				175				
gga	aca	cca	gaa	agg	tcc	agt	gac	agg	ccc	cga	ggt	cac	agg	gca	ggg	576	
Gly	Thr	Pro	Glu	Arg	Ser	Ser	Asp	Arg	Pro	Arg	Gly	His	Arg	Ala	Gly		
			180					185					190				

aaa tta gct aat gaa ctt att tct gct gat gtt cac gtc tgc acc ttc 624
 Lys Leu Ala Asn Glu Leu Ile Ser Ala Asp Val His Val Cys Thr Phe
 195 200 205

tac cct act ccc aag ccc tgt gca ggc ttt taa 657
 Tyr Pro Thr Pro Lys Pro Cys Ala Gly Phe *
 210 215

<210> 206
 <211> 218
 <212> PRT
 <213> Homo sapiens

<400> 206
 Met Arg Asp Lys Ala Ala Pro Ala Trp Thr Val Leu Ala Leu Met Gln
 1 5 10 15
 Gly Val Gln Ala Lys Lys Glu Arg Pro Ser Trp Leu Arg Asp Ala Val
 20 25 30
 Leu Cys Ser Thr Thr Pro Val Pro Arg Ala Phe Pro Met Ala Lys His
 35 40 45
 Gln His Leu Pro Leu Phe Lys Ser Leu Ser Val Ala Gln Gln Lys Thr
 50 55 60
 Arg His Asp Thr Tyr Leu Arg Phe Asn Ile Leu Ile Leu Arg Leu Tyr
 65 70 75 80
 Asn Thr Gly Tyr Tyr Trp Gln His His Glu Thr Lys Lys Gln Lys Leu
 85 90 95
 Leu Pro Thr Pro Pro His Val Thr Leu Gly Ile Gln Cys Arg Thr Val
 100 105 110
 Lys Asp Lys Ser Leu His Leu Ser Ser Ala Ile Leu Val Leu Ser Val
 115 120 125
 Thr Lys Gln Ser Val Arg Pro Leu Gln Arg Asn Gln His Leu Ala Asp
 130 135 140
 Ile Ser Thr Gly Ala Ala Thr Thr Cys Trp Pro Glu Glu Val Thr Leu
 145 150 155 160
 Val Ala Tyr Ser Val His Thr Glu Arg His Tyr Glu Asn Gln Gln Asn
 165 170 175
 Gly Thr Pro Glu Arg Ser Ser Asp Arg Pro Arg Gly His Arg Ala Gly
 180 185 190
 Lys Leu Ala Asn Glu Leu Ile Ser Ala Asp Val His Val Cys Thr Phe
 195 200 205
 Tyr Pro Thr Pro Lys Pro Cys Ala Gly Phe
 210 215

<210> 207
 <211> 354
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(354)

<400> 207

atg agc cca ggc tat ttg ctg ctg ctg ctg ctg ttg gag tca cct gtt	48
Met Ser Pro Gly Tyr Leu Leu Leu Leu Leu Leu Leu Glu Ser Pro Val	
1 5 10 15	
gct gga agg aac tgt gcc act gta cta cac cag aac agc tgc cat ctc	96
Ala Gly Arg Asn Cys Ala Thr Val Leu His Gln Asn Ser Cys His Leu	
20 25 30	
cat gac aac aag cac gcg ctg gtg ctg cct gcc tgg agg gga gaa gag	144
His Asp Asn Lys His Ala Leu Val Leu Pro Ala Trp Arg Gly Glu Glu	
35 40 45	
cac aga gaa ggc att agc tac tgc cct ccc aga cgc agg aca agc gac	192
His Arg Glu Gly Ile Ser Tyr Cys Pro Pro Arg Arg Arg Thr Ser Asp	
50 55 60	
aga att tcc aac agc atc ggc tac tac ggc aac acc ttt tta ctc ttg	240
Arg Ile Ser Asn Ser Ile Gly Tyr Tyr Gly Asn Thr Phe Leu Leu Leu	
65 70 75 80	
tgc acc aaa ctg gcc gac atc tcg gaa caa gga ggg gac tgg cct tcc	288
Cys Thr Lys Leu Ala Asp Ile Ser Glu Gln Gly Gly Asp Trp Pro Ser	
85 90 95	
cag atc cac aat gcc gcg gaa gca gag cca gcc gcc tct cca ctc tcc	336
Gln Ile His Asn Ala Ala Glu Ala Glu Pro Ala Ala Ser Pro Leu Ser	
100 105 110	
gcc aac cgc gac aag taa	354
Ala Asn Arg Asp Lys *	
115	

<400> 208

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<210> 209
<211> 693
<212> DNA
<213> Homo sapiens
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<400> 209

atg	ggc	tcc	ccg	gcc	acc	gcc	gcc	acc	ggg	ctc	ctc	ctc	ctg	ctg	ctg	48
Met	Gly	Ser	Pro	Ala	Thr	Ala	Ala	Thr	Gly	Leu	Leu	Leu	Leu	Leu	Leu	
1				5					10					15		
ctg	ctg	ctg	ctg	ctg	ccg	ccg	cgg	ctc	ggc	cgg	gag	aga	aaa	ggg	ctg	96
Leu	Leu	Leu	Leu	Leu	Pro	Pro	Arg	Leu	Gly	Arg	Glu	Arg	Lys	Gly	Leu	
				20					25					30		
agg	gaa	acg	tgg	tcc	ctt	ata	tta	ctt	tca	gcc	gtg	ggt	tgt	cct	gag	144

Arg	Glu	Thr	Trp	Ser	Leu	Ile	Leu	Leu	Ser	Ala	Val	Gly	Cys	Pro	Glu		
		35					40					45					
ctg	ata	gca	cgc	gat	gat	cga	tgg	ttg	gac	ctt	aac	tgc	cgt	act	cat	192	
Leu	Ile	Ala	Arg	Asp	Asp	Arg	Trp	Leu	Asp	Leu	Asn	Cys	Arg	Thr	His		
	50					55					60						
agt	gga	gac	act	atc	gca	tac	ccg	ttg	tcg	tgt	tcg	act	aat	ccc	gtt	240	
Ser	Gly	Asp	Thr	Ile	Ala	Tyr	Pro	Leu	Ser	Cys	Ser	Thr	Asn	Pro	Val		
	65				70					75					80		
cgc	ggc	ggc	ctt	gtc	aac	aac	gtg	ccc	ttt	ggc	cct	cca	tca	cga	atg	288	
Arg	Gly	Gly	Leu	Val	Asn	Asn	Val	Pro	Phe	Gly	Pro	Pro	Ser	Arg	Met		
				85					90					95			
tgc	agt	cat	tcg	atg	gct	gag	ggc	aag	atc	aca	cac	ttt	gtc	gtt	tct	336	
Cys	Ser	His	Ser	Met	Ala	Glu	Gly	Lys	Ile	Thr	His	Phe	Val	Val	Ser		
			100					105					110				
tct	act	ttg	gtg	gat	gtg	cct	cag	tgc	ccg	cat	ggc	gca	ctc	ctt	gca	384	
Ser	Thr	Leu	Val	Asp	Val	Pro	Gln	Cys	Pro	His	Gly	Ala	Leu	Leu	Ala		
			115				120					125					
ggc	ctc	cta	ctg	tgc	ctc	ccc	aag	gcc	act	gga	aga	acc	caa	act	gcc	432	
Gly	Leu	Leu	Leu	Cys	Leu	Pro	Lys	Ala	Thr	Gly	Arg	Thr	Gln	Thr	Ala		
	130					135					140						
atc	gga	ttt	cag	agt	gtc	ggc	gtc	tgc	gta	aga	tta	cgc	tcc	att	acc	480	
Ile	Gly	Phe	Gln	Ser	Val	Gly	Val	Cys	Val	Arg	Leu	Arg	Ser	Ile	Thr		
	145				150					155					160		
agt	agt	tgg	caa	gtt	cat	acg	ggc	cgc	cat	tgg	cac	gcc	atg	gag	ggc	528	
Ser	Ser	Trp	Gln	Val	His	Thr	Gly	Arg	His	Trp	His	Ala	Met	Glu	Gly		
				165				170						175			
tac	tac	aga	gat	aat	cct	ggc	tct	aaa	tca	tcg	gtg	acg	ggg	aca	gtc	576	
Tyr	Tyr	Arg	Asp	Asn	Pro	Gly	Ser	Lys	Ser	Ser	Val	Thr	Gly	Thr	Val		
			180					185					190				
tac	gac	atg	aca	tcc	tcc	aga	aaa	tcc	acc	gtg	ttg	gta	aag	gtg	ctc	624	
Tyr	Asp	Met	Thr	Ser	Ser	Arg	Lys	Ser	Thr	Val	Leu	Val	Lys	Val	Leu		
	195						200					205					

aaa aga cgg aat gct atc tct cgc tcg caa tgg tgt ctt tct cga gag 672
 Lys Arg Arg Asn Ala Ile Ser Arg Ser Gln Trp Cys Leu Ser Arg Glu
 210 215 220

gct ata gaa ggc aga aaa tag 693
 Ala Ile Glu Gly Arg Lys *
 225 230

<210> 210
 <211> 230
 <212> PRT
 <213> Homo sapiens

<400> 210
 Met Gly Ser Pro Ala Thr Ala Ala Thr Gly Leu Leu Leu Leu Leu Leu
 1 5 10 15
 Leu Leu Leu Leu Leu Pro Pro Arg Leu Gly Arg Glu Arg Lys Gly Leu
 20 25 30
 Arg Glu Thr Trp Ser Leu Ile Leu Leu Ser Ala Val Gly Cys Pro Glu
 35 40 45
 Leu Ile Ala Arg Asp Asp Arg Trp Leu Asp Leu Asn Cys Arg Thr His
 50 55 60
 Ser Gly Asp Thr Ile Ala Tyr Pro Leu Ser Cys Ser Thr Asn Pro Val
 65 70 75 80
 Arg Gly Gly Leu Val Asn Asn Val Pro Phe Gly Pro Pro Ser Arg Met
 85 90 95
 Cys Ser His Ser Met Ala Glu Gly Lys Ile Thr His Phe Val Val Ser
 100 105 110
 Ser Thr Leu Val Asp Val Pro Gln Cys Pro His Gly Ala Leu Leu Ala
 115 120 125
 Gly Leu Leu Leu Cys Leu Pro Lys Ala Thr Gly Arg Thr Gln Thr Ala
 130 135 140
 Ile Gly Phe Gln Ser Val Gly Val Cys Val Arg Leu Arg Ser Ile Thr
 145 150 155 160
 Ser Ser Trp Gln Val His Thr Gly Arg His Trp His Ala Met Glu Gly
 165 170 175
 Tyr Tyr Arg Asp Asn Pro Gly Ser Lys Ser Ser Val Thr Gly Thr Val
 180 185 190
 Tyr Asp Met Thr Ser Ser Arg Lys Ser Thr Val Leu Val Lys Val Leu
 195 200 205
 Lys Arg Arg Asn Ala Ile Ser Arg Ser Gln Trp Cys Leu Ser Arg Glu
 210 215 220

Ala Ile Glu Gly Arg Lys
225 230

<210> 211
<211> 307
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(307)

<400> 211

atg ctc ctg ctg ctg ctc ctt gaa aca ctg gct gtg ttt gca ctg agg 48
Met Leu Leu Leu Leu Leu Leu Glu Thr Leu Ala Val Phe Ala Leu Arg
1 5 10 15

cca tgc ctc agc cag cga ctg agt gtg aca agg att ctc agt cct gtt 96
Pro Cys Leu Ser Gln Arg Leu Ser Val Thr Arg Ile Leu Ser Pro Val
20 25 30

cct ggg aga tgt gag att cct ttg ctg gca aac ttc agc ttg aat att 144
Pro Gly Arg Cys Glu Ile Pro Leu Leu Ala Asn Phe Ser Leu Asn Ile
35 40 45

ccc cag gtt agc caa ttc cca gag ata ata caa caa ctt gct aca cta 192
Pro Gln Val Ser Gln Phe Pro Glu Ile Ile Gln Gln Leu Ala Thr Leu
50 55 60

gca tgc ttt tca ggt tca aat cta cca att caa agc cct tac acc caa 240
Ala Cys Phe Ser Gly Ser Asn Leu Pro Ile Gln Ser Pro Tyr Thr Gln
65 70 75 80

cca cct act tta tct ggc tct tgc act ctg ggt cac tat cca ctt gcc 288
Pro Pro Thr Leu Ser Gly Ser Cys Thr Leu Gly His Tyr Pro Leu Ala
85 90 95

cta atc acc tca gga cca g 307
Leu Ile Thr Ser Gly Pro
100

<210> 212

<211> 102
 <212> PRT
 <213> Homo sapiens

<400> 212

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Met Leu Leu Leu Leu Leu Leu Glu Thr Leu Ala Val Phe Ala Leu Arg
 1          5          10          15
Pro Cys Leu Ser Gln Arg Leu Ser Val Thr Arg Ile Leu Ser Pro Val
          20          25          30
Pro Gly Arg Cys Glu Ile Pro Leu Leu Ala Asn Phe Ser Leu Asn Ile
          35          40          45
Pro Gln Val Ser Gln Phe Pro Glu Ile Ile Gln Gln Leu Ala Thr Leu
          50          55          60
Ala Cys Phe Ser Gly Ser Asn Leu Pro Ile Gln Ser Pro Tyr Thr Gln
65          70          75          80
Pro Pro Thr Leu Ser Gly Ser Cys Thr Leu Gly His Tyr Pro Leu Ala
          85          90          95
Leu Ile Thr Ser Gly Pro
          100
  
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<210> 213
 <211> 615
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(615)

<400> 213

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atg tca cct cca agc acc tcc tgg ggt tgc ctg tcc tct ctc ctc ttc      48
Met Ser Pro Pro Ser Thr Ser Trp Gly Cys Leu Ser Ser Leu Leu Phe
 1          5          10          15

ctg ctg agc ccc tgg gtc caa gga cct ccc acc ttc aaa aaa gta aaa      96
Leu Leu Ser Pro Trp Val Gln Gly Pro Pro Thr Phe Lys Lys Val Lys
          20          25          30

aca gca cag ccc aga ccc agg ggt aaa att cat gtc atc act tct tcc      144
Thr Ala Gln Pro Arg Pro Arg Gly Lys Ile His Val Ile Thr Ser Ser
          35          40          45

tgg gcc agc acc caa ata cct cct gag cca cag gaa cac gat gcc tct      192
  
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Trp	Ala	Ser	Thr	Gln	Ile	Pro	Pro	Glu	Pro	Gln	Glu	His	Asp	Ala	Ser		
50						55					60						
gtg	gcc	ctg	aca	gcc	act	gcc	gat	tgt	cct	ggg	agg	ggc	ctt	cag	gga	240	
Val	Ala	Leu	Thr	Ala	Thr	Ala	Asp	Cys	Pro	Gly	Arg	Gly	Leu	Gln	Gly		
65					70				75					80			
acc	gca	cag	gaa	gga	ggg	tgc	agc	tca	gcc	cgt	ttt	caa	atc	cag	cag	288	
Thr	Ala	Gln	Glu	Gly	Gly	Cys	Ser	Ser	Ala	Arg	Phe	Gln	Ile	Gln	Gln		
				85				90						95			
gat	gtt	cat	gac	ctc	cct	gca	gac	act	aat	gga	cag	aac	gtc	aca	gca	336	
Asp	Val	His	Asp	Leu	Pro	Ala	Asp	Thr	Asn	Gly	Gln	Asn	Val	Thr	Ala		
			100					105					110				
gtc	tgc	ttc	cct	cac	ctg	tac	ggg	ggg	tac	ccc	aga	tca	ccc	cca	gtc	384	
Val	Cys	Phe	Pro	His	Leu	Tyr	Gly	Gly	Tyr	Pro	Arg	Ser	Pro	Pro	Val		
		115					120					125					
acc	gac	tgc	atg	caa	atc	tct	gtc	tca	gag	ttt	ggg	ccc	agc	aca	ttc	432	
Thr	Asp	Cys	Met	Gln	Ile	Ser	Val	Ser	Glu	Phe	Gly	Pro	Ser	Thr	Phe		
	130					135					140						
aac	cta	ggg	cat	gta	gga	cca	ccc	tcg	ttt	cac	gat	aaa	caa	cca	aaa	480	
Asn	Leu	Gly	His	Val	Gly	Pro	Pro	Ser	Phe	His	Asp	Lys	Gln	Pro	Lys		
145					150				155					160			
cag	ggc	agt	tac	gtg	atg	tgc	gta	aga	tgg	cac	gac	tca	cac	gtg	ccg	528	
Gln	Gly	Ser	Tyr	Val	Met	Cys	Val	Arg	Trp	His	Asp	Ser	His	Val	Pro		
				165				170						175			
cag	ctg	gaa	ctt	aaa	ctc	cat	ccg	gac	tcc	aag	gcc	acc	ctg	ttg	tct	576	
Gln	Leu	Glu	Leu	Lys	Leu	His	Pro	Asp	Ser	Lys	Ala	Thr	Leu	Leu	Ser		
			180					185					190				
ctc	cac	aat	caa	tgc	tca	gag	cac	agc	ctg	caa	ctg	taa				615	
Leu	His	Asn	Gln	Cys	Ser	Glu	His	Ser	Leu	Gln	Leu	*					
		195				200											

<210> 214

<211> 204

<212> PRT

<213> Homo sapiens

<400> 214

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Met Ser Pro Pro Ser Thr Ser Trp Gly Cys Leu Ser Ser Leu Leu Phe
 1          5          10          15
Leu Leu Ser Pro Trp Val Gln Gly Pro Pro Thr Phe Lys Lys Val Lys
 20          25          30
Thr Ala Gln Pro Arg Pro Arg Gly Lys Ile His Val Ile Thr Ser Ser
 35          40          45
Trp Ala Ser Thr Gln Ile Pro Pro Glu Pro Gln Glu His Asp Ala Ser
 50          55          60
Val Ala Leu Thr Ala Thr Ala Asp Cys Pro Gly Arg Gly Leu Gln Gly
 65          70          75          80
Thr Ala Gln Glu Gly Gly Cys Ser Ser Ala Arg Phe Gln Ile Gln Gln
 85          90          95
Asp Val His Asp Leu Pro Ala Asp Thr Asn Gly Gln Asn Val Thr Ala
100          105          110
Val Cys Phe Pro His Leu Tyr Gly Gly Tyr Pro Arg Ser Pro Pro Val
115          120          125
Thr Asp Cys Met Gln Ile Ser Val Ser Glu Phe Gly Pro Ser Thr Phe
130          135          140
Asn Leu Gly His Val Gly Pro Pro Ser Phe His Asp Lys Gln Pro Lys
145          150          155          160
Gln Gly Ser Tyr Val Met Cys Val Arg Trp His Asp Ser His Val Pro
165          170          175
Gln Leu Glu Leu Lys Leu His Pro Asp Ser Lys Ala Thr Leu Leu Ser
180          185          190
Leu His Asn Gln Cys Ser Glu His Ser Leu Gln Leu
195          200

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<210> 215

<211> 483

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(483)

<400> 215

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atg cct gat gtc tgg ggt cca gct gct gct gcc agt gct gcc tct tct
Met Pro Asp Val Trp Gly Pro Ala Ala Ala Ala Ser Ala Ala Ser Ser
 1          5          10          15

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gct gcc aac ccc act ctt ttc atc ctc ctg ctg ctt cca cca aca ttt 96
 Ala Ala Asn Pro Thr Leu Phe Ile Leu Leu Leu Leu Pro Pro Thr Phe
 20 25 30

ctg ctg cca tcg cca aaa tta cag atg ctg cca gca ctg cag ctt tgc 144
 Leu Leu Pro Ser Pro Lys Leu Gln Met Leu Pro Ala Leu Gln Leu Cys
 35 40 45

ttc ccc cct gct gtc ttg ttg ctg cat tgc cat ggc atc agg caa ggg 192
 Phe Pro Pro Ala Val Leu Leu Leu His Cys His Gly Ile Arg Gln Gly
 50 55 60

ttc agg ggc cta ggc aaa tgg act gtg gca ctt gta tgt ctc cct cct 240
 Phe Arg Gly Leu Gly Lys Trp Thr Val Ala Leu Val Cys Leu Pro Pro
 65 70 75 80

gga aaa tgc agg cta tcc aat aaa ggg gag aga gga aca ggg cag agc 288
 Gly Lys Cys Arg Leu Ser Asn Lys Gly Glu Arg Gly Thr Gly Gln Ser
 85 90 95

act ata aaa ggc aaa cac cgt ggt gaa att tgc agc acc atc cgg ctg 336
 Thr Ile Lys Gly Lys His Arg Gly Glu Ile Cys Ser Thr Ile Arg Leu
 100 105 110

cca aat tta gca tcc agg tca ctg gtg cca cgg aaa gcg ttg cca ctg 384
 Pro Asn Leu Ala Ser Arg Ser Leu Val Pro Arg Lys Ala Leu Pro Leu
 115 120 125

atg ctt gtg ccg gga aag gca cct ctc ctc tgc ttc agt gtc cat gct 432
 Met Leu Val Pro Gly Lys Ala Pro Leu Leu Cys Phe Ser Val His Ala
 130 135 140

aag gga aac cta atg cct cac act gac aaa aat gca ccc agt gga tct 480
 Lys Gly Asn Leu Met Pro His Thr Asp Lys Asn Ala Pro Ser Gly Ser
 145 150 155 160

taa 483
 *

217

<211> 160
<212> PRT
<213> Homo sapiens

<400> 216

Met Pro Asp Val Trp Gly Pro Ala Ala Ala Ser Ala Ala Ser Ser
1 5 10 15
Ala Ala Asn Pro Thr Leu Phe Ile Leu Leu Leu Leu Pro Pro Thr Phe
20 25 30
Leu Leu Pro Ser Pro Lys Leu Gln Met Leu Pro Ala Leu Gln Leu Cys
35 40 45
Phe Pro Pro Ala Val Leu Leu Leu His Cys His Gly Ile Arg Gln Gly
50 55 60
Phe Arg Gly Leu Gly Lys Trp Thr Val Ala Leu Val Cys Leu Pro Pro
65 70 75 80
Gly Lys Cys Arg Leu Ser Asn Lys Gly Glu Arg Gly Thr Gly Gln Ser
85 90 95
Thr Ile Lys Gly Lys His Arg Gly Glu Ile Cys Ser Thr Ile Arg Leu
100 105 110
Pro Asn Leu Ala Ser Arg Ser Leu Val Pro Arg Lys Ala Leu Pro Leu
115 120 125
Met Leu Val Pro Gly Lys Ala Pro Leu Leu Cys Phe Ser Val His Ala
130 135 140
Lys Gly Asn Leu Met Pro His Thr Asp Lys Asn Ala Pro Ser Gly Ser
145 150 155 160

<210> 217
<211> 240
<212> DNA
<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(240)

<400> 217

atg acc aac aga ttc ttg ctc ctg tta tct tct ttc cag cag gtc tat 48
Met Thr Asn Arg Phe Leu Leu Leu Leu Ser Ser Phe Gln Gln Val Tyr
1 5 10 15
ggg gac cgt aaa act gtt aaa gac ttt tgt tca ggc tcc ctc aac agt 96
Gly Asp Arg Lys Thr Val Lys Asp Phe Cys Ser Gly Ser Leu Asn Ser
20 25 30

1					5					10					15					
caa	gcc	ctc	agg	gct	ctg	cag	gac	aat	cct	cgg	cgt	ctg	ctg	ctg	ctg		96			
Gln	Ala	Leu	Arg	Ala	Leu	Gln	Asp	Asn	Pro	Arg	Arg	Leu	Leu	Leu	Leu					
			20				25						30							
ctg	ctg	ctg	ctg	gaa	cct	tct	cag	ggc	gtc	ctc	tgc	tgg	cag	gca	ggc		144			
Leu	Leu	Leu	Leu	Glu	Pro	Ser	Gln	Gly	Val	Leu	Cys	Trp	Gln	Ala	Gly					
			35				40						45							
ttc	gca	cac	agc	ctc	tgc	cag	ggc	tgt	gca	cag	cag	gca	gca	cca	ggc		192			
Phe	Ala	His	Ser	Leu	Cys	Gln	Gly	Cys	Ala	Gln	Gln	Ala	Ala	Pro	Gly					
			50				55						60							
cac	agc	att	gac	tgg	cta	ttt	gtg	caa	cgc	tgg	ttg	aag	acg	cca	gtg		240			
His	Ser	Ile	Asp	Trp	Leu	Phe	Val	Gln	Arg	Trp	Leu	Lys	Thr	Pro	Val					
			65				70						75			80				
acc	tgg	aaa	agg	gcc	caa	gcc	agg	ccg	cgg	ccg	cgg	ctc	ctc	gac	tcc		288			
Thr	Trp	Lys	Arg	Ala	Gln	Ala	Arg	Pro	Arg	Pro	Arg	Leu	Leu	Asp	Ser					
			85						90						95					
tcc	ggt	cac	ctg	gcc	cca	gcc	tgg	gac	cgc	tcc	cgc	ctc	cag	ccg	ctg		336			
Ser	Gly	His	Leu	Ala	Pro	Ala	Trp	Asp	Arg	Ser	Arg	Leu	Gln	Pro	Leu					
			100						105						110					
gaa	agc	atc	tcc	agg	ctg	gtg	gcg	cgg	act	ttc	atg	gaa	aca	tca	cct		384			
Glu	Ser	Ile	Ser	Arg	Leu	Val	Ala	Arg	Thr	Phe	Met	Glu	Thr	Ser	Pro					
			115						120						125					
ctc	ttc	aaa	gga	tcc	ttg	gat	ccc	cca	aaa	gag	aac	acc	agc	tct	ggg		432			
Leu	Phe	Lys	Gly	Ser	Leu	Asp	Pro	Pro	Lys	Glu	Asn	Thr	Ser	Ser	Gly					
			130						135						140					
atc	gcc	agg	ccc	tgg	ctc	agc	tct	cca	ccc	tgt	aat	gaa	atg	gcc	agc		480			
Ile	Ala	Arg	Pro	Trp	Leu	Ser	Ser	Pro	Pro	Cys	Asn	Glu	Met	Ala	Ser					
			145						150						155		160			
tat	ctg	gga	cat	tac	tgt	agc	ctc	ctc	gcc	atc	aga	act	gtc	act	ccc		528			
Tyr	Leu	Gly	His	Tyr	Cys	Ser	Leu	Leu	Ala	Ile	Arg	Thr	Val	Thr	Pro					
			165						170						175					
gct	gcc	atc	atc	ctc	tcc	ttc	agc	acc	atc	tcc	att	ctc	atc	act	cgc		576			

Ala Ala Ile Ile Leu Ser Phe Ser Thr Ile Ser Ile Leu Ile Thr Arg
 180 185 190

atc acc acc acc tca cac aga acc atc tgc atc ctt ctg ctc acc cag 624
 Ile Thr Thr Thr Ser His Arg Thr Ile Cys Ile Leu Leu Leu Thr Gln
 195 200 205

tgg acc ctc ttc tcc ctg tac cca ggg agg aac cct atc agc att tgc 672
 Trp Thr Leu Phe Ser Leu Tyr Pro Gly Arg Asn Pro Ile Ser Ile Cys
 210 215 220

tgc ctt tga 681
 Cys Leu *
 225

<210> 220
 <211> 226
 <212> PRT
 <213> Homo sapiens

<400> 220
 Met Asn Leu Gln His Gln Pro Leu Pro Val Ser His Ser Gln Gly Gly
 1 5 10 15
 Gln Ala Leu Arg Ala Leu Gln Asp Asn Pro Arg Arg Leu Leu Leu Leu
 20 25 30
 Leu Leu Leu Leu Glu Pro Ser Gln Gly Val Leu Cys Trp Gln Ala Gly
 35 40 45
 Phe Ala His Ser Leu Cys Gln Gly Cys Ala Gln Gln Ala Ala Pro Gly
 50 55 60
 His Ser Ile Asp Trp Leu Phe Val Gln Arg Trp Leu Lys Thr Pro Val
 65 70 75 80
 Thr Trp Lys Arg Ala Gln Ala Arg Pro Arg Pro Arg Leu Leu Asp Ser
 85 90 95
 Ser Gly His Leu Ala Pro Ala Trp Asp Arg Ser Arg Leu Gln Pro Leu
 100 105 110
 Glu Ser Ile Ser Arg Leu Val Ala Arg Thr Phe Met Glu Thr Ser Pro
 115 120 125
 Leu Phe Lys Gly Ser Leu Asp Pro Pro Lys Glu Asn Thr Ser Ser Gly
 130 135 140
 Ile Ala Arg Pro Trp Leu Ser Ser Pro Pro Cys Asn Glu Met Ala Ser
 145 150 155 160
 Tyr Leu Gly His Tyr Cys Ser Leu Leu Ala Ile Arg Thr Val Thr Pro

165 170 175
 Ala Ala Ile Ile Leu Ser Phe Ser Thr Ile Ser Ile Leu Ile Thr Arg
 180 185 190
 Ile Thr Thr Thr Ser His Arg Thr Ile Cys Ile Leu Leu Leu Thr Gln
 195 200 205
 Trp Thr Leu Phe Ser Leu Tyr Pro Gly Arg Asn Pro Ile Ser Ile Cys
 210 215 220
 Cys Leu
 225

<210> 221
 <211> 441
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(441)

<400> 221

atg aca agg ctt ttt tgg ctg tgt gtg tcc agc tgt tcc atg cca gga 48
 Met Thr Arg Leu Phe Trp Leu Cys Val Ser Ser Cys Ser Met Pro Gly
 1 5 10 15

gga gga gga gtt aca tgc tgg aag ctt gca gat agc ctg ggg ctg ctg 96
 Gly Gly Gly Val Thr Cys Trp Lys Leu Ala Asp Ser Leu Gly Leu Leu
 20 25 30

ctc gcc ttg ctg cgg ttg gtg gca gct acc gag act acc tcg cac cag 144
 Leu Ala Leu Leu Arg Leu Val Ala Ala Thr Glu Thr Thr Ser His Gln
 35 40 45

agc ggc ctg gcc ggg cag gcc ccg cag cgc tcc tac tcc ctc ttc ccg 192
 Ser Gly Leu Ala Gly Gln Ala Pro Gln Arg Ser Tyr Ser Leu Phe Pro
 50 55 60

gcc cct gga ctt gcg gct gct gcc aca act agc gca gat gtc act ata 240
 Ala Pro Gly Leu Ala Ala Ala Ala Thr Thr Ser Ala Asp Val Thr Ile
 65 70 75 80

acc atc gct gct gtt gcc ctc aat gca ctg gcc cac cct aca aag ctc 288
 Thr Ile Ala Ala Val Ala Leu Asn Ala Leu Ala His Pro Thr Lys Leu
 85 90 95

cta cta cct ggc cac cgc cgc agc cct gcc cct gcc atg gcc aca gct 336
 Leu Leu Pro Gly His Arg Arg Ser Pro Ala Pro Ala Met Ala Thr Ala
 100 105 110

ggc cgt cct cct acc gct ctg gtg cga ggt agt ctc ggt agc tgc cac 384
 Gly Arg Pro Pro Thr Ala Leu Val Arg Gly Ser Leu Gly Ser Cys His
 115 120 125

caa ccg cag caa ggc gag cag cag ccc cta ggc tat ctg caa gct tcc 432
 Gln Pro Gln Gln Gly Glu Gln Gln Pro Leu Gly Tyr Leu Gln Ala Ser
 130 135 140

agc atg taa 441
 Ser Met *
 145

<210> 222
 <211> 146
 <212> PRT
 <213> Homo sapiens

<400> 222

Met Thr Arg Leu Phe Trp Leu Cys Val Ser Ser Cys Ser Met Pro Gly
 1 5 10 15
 Gly Gly Gly Val Thr Cys Trp Lys Leu Ala Asp Ser Leu Gly Leu Leu
 20 25 30
 Leu Ala Leu Leu Arg Leu Val Ala Ala Thr Glu Thr Thr Ser His Gln
 35 40 45
 Ser Gly Leu Ala Gly Gln Ala Pro Gln Arg Ser Tyr Ser Leu Phe Pro
 50 55 60
 Ala Pro Gly Leu Ala Ala Ala Ala Thr Thr Ser Ala Asp Val Thr Ile
 65 70 75 80
 Thr Ile Ala Ala Val Ala Leu Asn Ala Leu Ala His Pro Thr Lys Leu
 85 90 95
 Leu Leu Pro Gly His Arg Arg Ser Pro Ala Pro Ala Met Ala Thr Ala
 100 105 110
 Gly Arg Pro Pro Thr Ala Leu Val Arg Gly Ser Leu Gly Ser Cys His
 115 120 125
 Gln Pro Gln Gln Gly Glu Gln Gln Pro Leu Gly Tyr Leu Gln Ala Ser
 130 135 140
 Ser Met

gtg aag gtt ttg tgt cag ccc cag gag ctg gat ggt tca ggt ccc atg	384
Val Lys Val Leu Cys Gln Pro Gln Glu Leu Asp Gly Ser Gly Pro Met	
115 120 125	
cag gga cgt gga ctt gtg cct gct cag cgc cgg cac tgt tct ttc agc	432
Gln Gly Arg Gly Leu Val Pro Ala Gln Arg Arg His Cys Ser Phe Ser	
130 135 140	
atc tac gag aag ctg atc cag ttc tgt gcc att gac gag ctt ggc acc	480
Ile Tyr Glu Lys Leu Ile Gln Phe Cys Ala Ile Asp Glu Leu Gly Thr	
145 150 155 160	
aac tac cca aag gat atg ttt gat ccc cat ggc tgg tct gag gac tcc	528
Asn Tyr Pro Lys Asp Met Phe Asp Pro His Gly Trp Ser Glu Asp Ser	
165 170 175	
tac tat gag gca tta gcc aag gcc cag aaa att gag atg gac aaa ttg	576
Tyr Tyr Glu Ala Leu Ala Lys Ala Gln Lys Ile Glu Met Asp Lys Leu	
180 185 190	
gaa aag gcc aaa aag gag cga aca aaa att gag ttt gtg acg ggc acc	624
Glu Lys Ala Lys Lys Glu Arg Thr Lys Ile Glu Phe Val Thr Gly Thr	
195 200 205	
aaa aaa ggc acc acg acc aac gcc acg tcc acc acc act acc act gcc	672
Lys Lys Gly Thr Thr Thr Asn Ala Thr Ser Thr Thr Thr Thr Ala	
210 215 220	
agc aca gct gtt gca gat gct cag aag aga aag agc aag tgg gat tcg	720
Ser Thr Ala Val Ala Asp Ala Gln Lys Arg Lys Ser Lys Trp Asp Ser	
225 230 235 240	
gct atc cca gtg aca acg ata gcc cag ccc acc atc ctc acc acc aca	768
Ala Ile Pro Val Thr Thr Ile Ala Gln Pro Thr Ile Leu Thr Thr Thr	
245 250 255	
gcc acc ctg cca gct gtt gtc acg gtc acc acc agc gcc agc ggc tcc	816
Ala Thr Leu Pro Ala Val Val Thr Val Thr Thr Ser Ala Ser Gly Ser	
260 265 270	
aag acc acc gtc atc tct gct gtg ggc acc att gtg aag aag gcc aag	864
Lys Thr Thr Val Ile Ser Ala Val Gly Thr Ile Val Lys Lys Ala Lys	

275

280

285

cag tga

870

Gln *

<210> 226

<211> 289

<212> PRT

<213> Homo sapiens

<400> 226

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Met Asn Ser Ala Phe Leu Leu Leu Phe Ala Cys Ile Leu Thr Ala Leu
 1          5          10          15
Leu Ser Ala Ser Cys Leu Phe Lys Gly Ile Asp Asn Thr Glu Ala Glu
          20          25          30
Lys Arg Asp Pro Gln Glu Leu Val Ala Ser Phe Ser Glu Arg Val Arg
          35          40          45
Asn Met Ser Pro Asp Glu Ile Lys Ile Pro Pro Glu Pro Pro Gly Arg
 50          55          60
Cys Ser Asn His Leu Gln Asn His Val Thr Leu Arg Ala Arg Gln Pro
65          70          75          80
Asp Asn Lys Leu Gln Pro Leu Thr Gly Pro Ser Pro Trp Glu Ser Gly
          85          90          95
Gly Pro Ser Gly Ser Leu Leu Arg Ala Ala Glu Leu Asp Leu Lys Val
          100          105          110
Val Lys Val Leu Cys Gln Pro Gln Glu Leu Asp Gly Ser Gly Pro Met
          115          120          125
Gln Gly Arg Gly Leu Val Pro Ala Gln Arg Arg His Cys Ser Phe Ser
          130          135          140
Ile Tyr Glu Lys Leu Ile Gln Phe Cys Ala Ile Asp Glu Leu Gly Thr
145          150          155          160
Asn Tyr Pro Lys Asp Met Phe Asp Pro His Gly Trp Ser Glu Asp Ser
          165          170          175
Tyr Tyr Glu Ala Leu Ala Lys Ala Gln Lys Ile Glu Met Asp Lys Leu
          180          185          190
Glu Lys Ala Lys Lys Glu Arg Thr Lys Ile Glu Phe Val Thr Gly Thr
          195          200          205
Lys Lys Gly Thr Thr Thr Asn Ala Thr Ser Thr Thr Thr Thr Ala
          210          215          220
Ser Thr Ala Val Ala Asp Ala Gln Lys Arg Lys Ser Lys Trp Asp Ser
225          230          235          240

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<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(768)

<400> 231

atg	cgc	ccc	cga	gcc	cca	gcc	tgc	gcc	gcc	gcg	gcg	ctc	ggg	ctc	tgc	48
Met	Arg	Pro	Arg	Ala	Pro	Ala	Cys	Ala	Ala	Ala	Ala	Leu	Gly	Leu	Cys	
1				5				10					15			

agc	ctt	ctg	ctg	ctg	ctc	gcg	ccc	ggg	cac	gcg	tgc	ccc	gcg	ggc	tgc	96
Ser	Leu	Leu	Leu	Leu	Leu	Ala	Pro	Gly	His	Ala	Cys	Pro	Ala	Gly	Cys	
			20					25					30			

gcc	tgc	acc	gac	ccg	cac	acc	gtg	gac	tgc	cgc	gac	cgc	ggg	ctg	ccc	144
Ala	Cys	Thr	Asp	Pro	His	Thr	Val	Asp	Cys	Arg	Asp	Arg	Gly	Leu	Pro	
		35					40					45				

agc	gtg	cca	gac	cct	ttc	ccc	ctg	gac	gtg	cgc	aag	ctg	ctg	gtg	gcc	192
Ser	Val	Pro	Asp	Pro	Phe	Pro	Leu	Asp	Val	Arg	Lys	Leu	Leu	Val	Ala	
	50					55					60					

ggc	aac	cgc	atc	cag	cgg	atc	ccc	gag	gac	ttc	ttc	atc	ttc	tac	ggc	240
Gly	Asn	Arg	Ile	Gln	Arg	Ile	Pro	Glu	Asp	Phe	Phe	Ile	Phe	Tyr	Gly	
65					70					75					80	

gac	ctg	gtc	tac	ctg	gac	ttc	agg	aac	aac	tcg	ctg	cgc	tcg	ctg	gag	288
Asp	Leu	Val	Tyr	Leu	Asp	Phe	Arg	Asn	Asn	Ser	Leu	Arg	Ser	Leu	Glu	
				85					90					95		

gag	ggc	acg	ttc	agc	ggc	tcg	gcc	aag	ctc	gtg	ttc	ctc	gac	ctc	agc	336
Glu	Gly	Thr	Phe	Ser	Gly	Ser	Ala	Lys	Leu	Val	Phe	Leu	Asp	Leu	Ser	
			100					105					110			

tac	aac	aac	ttg	acc	cag	ctg	ggc	gcc	ggc	gcc	ttc	cgc	tcg	gcc	ggg	384
Tyr	Asn	Asn	Leu	Thr	Gln	Leu	Gly	Ala	Gly	Ala	Phe	Arg	Ser	Ala	Gly	
			115				120					125				

agg	ctg	gtg	aag	ctt	agc	ctg	gct	aac	aac	aac	ctg	gtg	ggc	gtg	cac	432
Arg	Leu	Val	Lys	Leu	Ser	Leu	Ala	Asn	Asn	Asn	Leu	Val	Gly	Val	His	
	130						135					140				

gag gac gcc ttc gag acc ctg gag tcg ctg cag gtg ctg gag ctc aac 480
 Glu Asp Ala Phe Glu Thr Leu Glu Ser Leu Gln Val Leu Glu Leu Asn
 145 150 155 160

gac aac aac ctg cgc agc ctc agc gtg gcc gcc ctg gcc gcg ctg ccc 528
 Asp Asn Asn Leu Arg Ser Leu Ser Val Ala Ala Leu Ala Ala Leu Pro
 165 170 175

gcg ctg cgc tcc ctg cgt ctg gac ggg aac ccc tgg ctg tgc gac tgt 576
 Ala Leu Arg Ser Leu Arg Leu Asp Gly Asn Pro Trp Leu Cys Asp Cys
 180 185 190

gac ttc gcc cac ctc ttc tcc tgg atc cag gag aac gca tcc aaa ctg 624
 Asp Phe Ala His Leu Phe Ser Trp Ile Gln Glu Asn Ala Ser Lys Leu
 195 200 205

ccc aaa gga ctg gcg ggt gtg gat tac tta tgc gtc cct ggt aag cgg 672
 Pro Lys Gly Leu Ala Gly Val Asp Tyr Leu Cys Val Pro Gly Lys Arg
 210 215 220

aat gca gcc tac tct atg gga aac ggc cgt att ctc agt acc gtg cac 720
 Asn Ala Ala Tyr Ser Met Gly Asn Gly Arg Ile Leu Ser Thr Val His
 225 230 235 240

ggg gag tca gcc agt tcc aag ggc tct cca gca gct tcc cga gcc taa 768
 Gly Glu Ser Ala Ser Ser Lys Gly Ser Pro Ala Ala Ser Arg Ala *
 245 250 255

<210> 232

<211> 255

<212> PRT

<213> Homo sapiens

<400> 232

Met Arg Pro Arg Ala Pro Ala Cys Ala Ala Ala Ala Leu Gly Leu Cys
 1 5 10 15
 Ser Leu Leu Leu Leu Leu Ala Pro Gly His Ala Cys Pro Ala Gly Cys
 20 25 30
 Ala Cys Thr Asp Pro His Thr Val Asp Cys Arg Asp Arg Gly Leu Pro
 35 40 45
 Ser Val Pro Asp Pro Phe Pro Leu Asp Val Arg Lys Leu Leu Val Ala

50 55 60
 Gly Asn Arg Ile Gln Arg Ile Pro Glu Asp Phe Phe Ile Phe Tyr Gly
 65 70 75 80
 Asp Leu Val Tyr Leu Asp Phe Arg Asn Asn Ser Leu Arg Ser Leu Glu
 85 90 95
 Glu Gly Thr Phe Ser Gly Ser Ala Lys Leu Val Phe Leu Asp Leu Ser
 100 105 110
 Tyr Asn Asn Leu Thr Gln Leu Gly Ala Gly Ala Phe Arg Ser Ala Gly
 115 120 125
 Arg Leu Val Lys Leu Ser Leu Ala Asn Asn Asn Leu Val Gly Val His
 130 135 140
 Glu Asp Ala Phe Glu Thr Leu Glu Ser Leu Gln Val Leu Glu Leu Asn
 145 150 155 160
 Asp Asn Asn Leu Arg Ser Leu Ser Val Ala Ala Leu Ala Ala Leu Pro
 165 170 175
 Ala Leu Arg Ser Leu Arg Leu Asp Gly Asn Pro Trp Leu Cys Asp Cys
 180 185 190
 Asp Phe Ala His Leu Phe Ser Trp Ile Gln Glu Asn Ala Ser Lys Leu
 195 200 205
 Pro Lys Gly Leu Ala Gly Val Asp Tyr Leu Cys Val Pro Gly Lys Arg
 210 215 220
 Asn Ala Ala Tyr Ser Met Gly Asn Gly Arg Ile Leu Ser Thr Val His
 225 230 235 240
 Gly Glu Ser Ala Ser Ser Lys Gly Ser Pro Ala Ala Ser Arg Ala
 245 250 255

<210> 233
 <211> 615
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(615)

<400> 233

atg tca cct cca agc acc tcc tgg ggt tgc ctg tcc tct ctc ctc ttc 48
 Met Ser Pro Pro Ser Thr Ser Trp Gly Cys Leu Ser Ser Leu Leu Phe
 1 5 10 15

ctg ctg agc ccc tgg gtc caa gga cct ccc acc ttc aaa aaa gta aaa 96
 Leu Leu Ser Pro Trp Val Gln Gly Pro Pro Thr Phe Lys Lys Val Lys
 20 25 30

aca Thr	gca Ala	cag Gln	ccc Pro	aga Arg	ccc Pro	agg Arg	ggt Gly	aaa Lys	att Ile	cat His	gtc Val	atc Ile	act Thr	tct Ser	tcc Ser	144	
35						40						45					
tgg Trp	gcc Ala	agc Ser	acc Thr	caa Gln	ata Ile	cct Pro	cct Pro	gag Glu	cca Pro	cag Gln	gaa Glu	cac His	gat Asp	gcc Ala	tct Ser	192	
50						55						60					
gtg Val	gcc Ala	ctg Leu	aca Thr	gcc Ala	act Thr	gcc Ala	gat Asp	tgt Cys	cct Pro	ggg Gly	agg Arg	ggc Gly	ctt Leu	cag Gln	gga Gly	240	
65			70						75						80		
acc Thr	gca Ala	cag Gln	gaa Glu	gga Gly	ggg Gly	tgc Cys	agc Ser	tca Ser	gcc Ala	cgt Arg	ttt Phe	caa Gln	atc Ile	cag Gln	cag Gln	288	
			85						90						95		
gat Asp	gtt Val	cat His	gac Asp	ctc Leu	cct Pro	gca Ala	gac Asp	act Thr	aat Asn	gga Gly	cag Gln	aac Asn	gtc Val	aca Thr	gca Ala	336	
			100						105						110		
gtc Val	tgc Cys	ttc Phe	cct Pro	cac His	ctg Leu	tac Tyr	ggg Gly	ggt Gly	tac Tyr	ccc Pro	aga Arg	tca Ser	ccc Pro	cca Pro	gtc Val	384	
115						120						125					
acc Thr	gac Asp	tgc Cys	atg Met	caa Gln	atc Ile	tct Ser	gtc Val	tca Ser	gag Glu	ttt Phe	ggt Gly	ccc Pro	agc Ser	aca Thr	ttc Phe	432	
130						135						140					
aac Asn	cta Leu	ggg Gly	cat His	gta Val	gga Gly	cca Pro	ccc Pro	tcg Ser	ttt Phe	cac His	gat Asp	aaa Lys	caa Gln	cca Pro	aaa Lys	480	
145			150						155						160		
cag Gln	ggc Gly	agt Ser	tac Tyr	gtg Val	atg Met	tgc Cys	gta Val	aga Arg	tgg Trp	cac His	gac Asp	tca Ser	cac His	gtg Val	ccg Pro	528	
			165						170						175		
cag Gln	ctg Leu	gaa Glu	ctt Leu	aaa Lys	ctc Leu	cat His	ccg Pro	gac Asp	tcc Ser	aag Lys	gcc Ala	acc Thr	ctg Leu	ttg Leu	tct Ser	576	
			180						185						190		
ctc Leu	cac His	aat Asn	caa Gln	tgc Cys	tca Ser	gag Glu	cac His	agc Ser	ctg Leu	caa Gln	ctg Leu	taa *				615	

195

200

<210> 234

<211> 204

<212> PRT

<213> Homo sapiens

<400> 234

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Met Ser Pro Pro Ser Thr Ser Trp Gly Cys Leu Ser Ser Leu Leu Phe
 1          5          10          15
Leu Leu Ser Pro Trp Val Gln Gly Pro Pro Thr Phe Lys Lys Val Lys
 20          25          30
Thr Ala Gln Pro Arg Pro Arg Gly Lys Ile His Val Ile Thr Ser Ser
 35          40          45
Trp Ala Ser Thr Gln Ile Pro Pro Glu Pro Gln Glu His Asp Ala Ser
 50          55          60
Val Ala Leu Thr Ala Thr Ala Asp Cys Pro Gly Arg Gly Leu Gln Gly
65          70          75          80
Thr Ala Gln Glu Gly Gly Cys Ser Ser Ala Arg Phe Gln Ile Gln Gln
 85          90          95
Asp Val His Asp Leu Pro Ala Asp Thr Asn Gly Gln Asn Val Thr Ala
100          105          110
Val Cys Phe Pro His Leu Tyr Gly Gly Tyr Pro Arg Ser Pro Pro Val
115          120          125
Thr Asp Cys Met Gln Ile Ser Val Ser Glu Phe Gly Pro Ser Thr Phe
130          135          140
Asn Leu Gly His Val Gly Pro Pro Ser Phe His Asp Lys Gln Pro Lys
145          150          155          160
Gln Gly Ser Tyr Val Met Cys Val Arg Trp His Asp Ser His Val Pro
165          170          175
Gln Leu Glu Leu Lys Leu His Pro Asp Ser Lys Ala Thr Leu Leu Ser
180          185          190
Leu His Asn Gln Cys Ser Glu His Ser Leu Gln Leu
195          200

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<210> 235

<211> 597

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

Gly Thr Pro Leu Leu Phe
195

<210> 237
<211> 327
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(327)

<400> 237

atg ctg ctg ctg ctg ctg ctg ctg ctg ctg cta ctg ctg cta tta cca 48
Met Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Pro
1 5 10 15

cgt gag ccc acc ttt gtg cta atc aag act cgc atc act gcc tta aaa 96
Arg Glu Pro Thr Phe Val Leu Ile Lys Thr Arg Ile Thr Ala Leu Lys
20 25 30

agt ggg cat cct aaa acg tcc aag gaa aac atc agg gga cat gag atg 144
Ser Gly His Pro Lys Thr Ser Lys Glu Asn Ile Arg Gly His Glu Met
35 40 45

tca gat ggc cct cac aac caa gca ctc tgt ctt gaa gca cta gct aag 192
Ser Asp Gly Pro His Asn Gln Ala Leu Cys Leu Glu Ala Leu Ala Lys
50 55 60

ctg cga atc aag ctg ctt att tgg tta gga gaa cct gtg aaa gac cat 240
Leu Arg Ile Lys Leu Leu Ile Trp Leu Gly Glu Pro Val Lys Asp His
65 70 75 80

agc ttg cat gcc ctg cgg ttc gac tct aga aga tcc ccc cca gca ggc 288
Ser Leu His Ala Leu Arg Phe Asp Ser Arg Arg Ser Pro Pro Ala Gly
85 90 95

cag att gta gta gtt ccc aac ttt ggc tgc aca ttg taa 327
Gln Ile Val Val Val Pro Asn Phe Gly Cys Thr Leu *
100 105

<210> 238

<211> 108
 <212> PRT
 <213> Homo sapiens

<400> 238

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Met Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Pro
 1          5          10          15
Arg Glu Pro Thr Phe Val Leu Ile Lys Thr Arg Ile Thr Ala Leu Lys
          20          25          30
Ser Gly His Pro Lys Thr Ser Lys Glu Asn Ile Arg Gly His Glu Met
          35          40          45
Ser Asp Gly Pro His Asn Gln Ala Leu Cys Leu Glu Ala Leu Ala Lys
          50          55          60
Leu Arg Ile Lys Leu Leu Ile Trp Leu Gly Glu Pro Val Lys Asp His
65          70          75          80
Ser Leu His Ala Leu Arg Phe Asp Ser Arg Arg Ser Pro Pro Ala Gly
          85          90          95
Gln Ile Val Val Val Pro Asn Phe Gly Cys Thr Leu
          100          105

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<210> 239
 <211> 456
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(456)

<400> 239

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atg cct gct tca gac acc agc ccc ctt ctt cgc ctc atc gca ctg agt      48
Met Pro Ala Ser Asp Thr Ser Pro Leu Leu Arg Leu Ile Ala Leu Ser
 1          5          10          15

agt aac atc att gca att gtt ttt cta ata gac tgc tgt gtc tgc cca      96
Ser Asn Ile Ile Ala Ile Val Phe Leu Ile Asp Cys Cys Val Cys Pro
          20          25          30

cta gat ttc aag ctc tct aaa gag gcc cac gat agt gtc act caa atc      144
Leu Asp Phe Lys Leu Ser Lys Glu Ala His Asp Ser Val Thr Gln Ile
          35          40          45

ctc tcc aga cag ccc ttt gga aac ata ttc cat gtt cct ctt ctt agg      192

```


65 70 75 80
 Gln Val Asn Thr Tyr His Tyr Gln Arg Ile Leu Leu Gly Ile Ser Ser
 85 90 95
 Asp Asn Ala Ile Leu Leu Glu Glu Glu Ser Glu Glu Gly Arg Pro Met
 100 105 110
 His Ile Ser Thr Ile Lys Glu Pro Ser Pro Asp Ser Pro Ile Leu Tyr
 115 120 125
 Leu Thr Leu Asn Leu Lys Leu Leu Thr Ser Arg Glu Glu Gly Val Tyr
 130 135 140
 Ser Arg Ala Thr Arg Lys Trp
 145 150

<210> 241
 <211> 579
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(579)

<400> 241

atg tat agc gcc gat ttt ggc ctg ctt gca ctg cta ccg ctg ccg agc 48
 Met Tyr Ser Ala Asp Phe Gly Leu Leu Ala Leu Leu Pro Leu Pro Ser
 1 5 10 15

caa ggc gcg ccg atg gcc acg acg ccc tta ccg ggc gcc cct acc cca 96
 Gln Gly Ala Pro Met Ala Thr Thr Pro Leu Pro Gly Ala Pro Thr Pro
 20 25 30

tgg gat gtt gcg att aca acc aac tgg acc ggc gct tac cgc aaa gaa 144
 Trp Asp Val Ala Ile Thr Thr Asn Trp Thr Gly Ala Tyr Arg Lys Glu
 35 40 45

tat gcc ctg cac gcg gct tgt acc ggg caa caa aaa aca aaa ata caa 192
 Tyr Ala Leu His Ala Ala Cys Thr Gly Gln Gln Lys Thr Lys Ile Gln
 50 55 60

aaa cgc gtg cgc ata gct ata cat gtt tgc ctg cgt act gca cca ctg 240
 Lys Arg Val Arg Ile Ala Ile His Val Cys Leu Arg Thr Ala Pro Leu
 65 70 75 80

gat aac cta tgt aca gga ttt gct gta aac ccg cct tgg cca cct gcc 288
 Asp Asn Leu Cys Thr Gly Phe Ala Val Asn Pro Pro Trp Pro Pro Ala

50	55	60	
gtc ctg ctg ctg ggc ctt gag gaa gcc aag att ctc tgc aat gac tgt			240
Val Leu Leu Leu Gly Leu Glu Glu Ala Lys Ile Leu Cys Asn Asp Cys			
65	70	75	80
aat gga cga tcc act gtt cag ttt cat ata tta ggc atg aaa tgt aag			288
Asn Gly Arg Ser Thr Val Gln Phe His Ile Leu Gly Met Lys Cys Lys			
	85	90	95
att tgt gaa tcc tat aat act gct caa gct gga gga cgt aga att tca			336
Ile Cys Glu Ser Tyr Asn Thr Ala Gln Ala Gly Gly Arg Arg Ile Ser			
	100	105	110
ctg gat cag caa tga			351
Leu Asp Gln Gln *			
	115		

<210> 244

<211> 116

<212> PRT

<213> Homo sapiens

<400> 244

Met Ala Arg Arg His Cys Phe Ser Tyr Trp Leu Leu Val Cys Trp Leu			
1	5	10	15
Val Val Thr Val Ala Glu Gly Gln Glu Glu Val Phe Thr Pro Pro Gly			
	20	25	30
Asp Ser Gln Asn Asn Ala Asp Ala Thr Asp Cys Gln Ile Phe Thr Leu			
	35	40	45
Thr Pro Pro Pro Ala Pro Arg Ser Pro Phe Cys Ser Glu Lys Gly Pro			
	50	55	60
Val Leu Leu Leu Gly Leu Glu Glu Ala Lys Ile Leu Cys Asn Asp Cys			
65	70	75	80
Asn Gly Arg Ser Thr Val Gln Phe His Ile Leu Gly Met Lys Cys Lys			
	85	90	95
Ile Cys Glu Ser Tyr Asn Thr Ala Gln Ala Gly Gly Arg Arg Ile Ser			
	100	105	110
Leu Asp Gln Gln			
	115		

<210> 245

F00350"424660

<211> 327
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(327)

<400> 245

atg	ctc	ctg	ctg	ctg	ctc	ctt	gaa	aca	ctg	gct	gtg	ttt	gca	ctg	agg	48
Met	Leu	Leu	Leu	Leu	Leu	Leu	Glu	Thr	Leu	Ala	Val	Phe	Ala	Leu	Arg	
1				5					10					15		

cca	tgc	ctc	agc	cag	cga	ctg	agt	gtg	aca	agg	att	ctc	agt	cct	gtt	96
Pro	Cys	Leu	Ser	Gln	Arg	Leu	Ser	Val	Thr	Arg	Ile	Leu	Ser	Pro	Val	
			20					25						30		

cct	ggg	aga	tgt	gag	att	cct	ttg	ctg	gca	aac	ttc	agc	ttg	aat	att	144
Pro	Gly	Arg	Cys	Glu	Ile	Pro	Leu	Leu	Ala	Asn	Phe	Ser	Leu	Asn	Ile	
		35					40					45				

ccc	cag	gta	caa	tgg	gat	acc	cgt	ggc	tac	act	cta	tca	cat	ctc	ttc	192
Pro	Gln	Val	Gln	Trp	Asp	Thr	Arg	Gly	Tyr	Thr	Leu	Ser	His	Leu	Phe	
	50					55					60					

att	cat	ctt	ctc	agc	aac	tct	cca	ttg	aac	act	tac	act	gtt	cta	gac	240
Ile	His	Leu	Leu	Ser	Asn	Ser	Pro	Leu	Asn	Thr	Tyr	Thr	Val	Leu	Asp	
65					70				75					80		

act	caa	gaa	aga	gca	ctc	ctt	aag	gca	gac	aaa	gtt	gcc	tgc	cct	caa	288
Thr	Gln	Glu	Arg	Ala	Leu	Leu	Lys	Ala	Asp	Lys	Val	Ala	Cys	Pro	Gln	
				85				90						95		

gaa	gct	act	att	cta	gtg	aaa	gaa	gac	aaa	caa	aaa	taa				327
Glu	Ala	Thr	Ile	Leu	Val	Lys	Glu	Asp	Lys	Gln	Lys	*				
			100				105									

<210> 246
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 246

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Met Leu Leu Leu Leu Leu Leu Glu Thr Leu Ala Val Phe Ala Leu Arg
 1          5          10          15
Pro Cys Leu Ser Gln Arg Leu Ser Val Thr Arg Ile Leu Ser Pro Val
          20          25          30
Pro Gly Arg Cys Glu Ile Pro Leu Leu Ala Asn Phe Ser Leu Asn Ile
          35          40          45
Pro Gln Val Gln Trp Asp Thr Arg Gly Tyr Thr Leu Ser His Leu Phe
          50          55          60
Ile His Leu Leu Ser Asn Ser Pro Leu Asn Thr Tyr Thr Val Leu Asp
65          70          75          80
Thr Gln Glu Arg Ala Leu Leu Lys Ala Asp Lys Val Ala Cys Pro Gln
          85          90          95
Glu Ala Thr Ile Leu Val Lys Glu Asp Lys Gln Lys
          100          105

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<210> 247

<211> 438

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(438)

<400> 247

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atg agt ttg ctg ttg ctg ctg ctg ctg ctg ctg ctg ttt aaa tgg      48
Met Ser Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Phe Lys Trp
 1          5          10          15

aaa aga aga gta gta agt ggt cat ctt ctc agc gtc tgg tgc tgg tcc      96
Lys Arg Arg Val Val Ser Gly His Leu Leu Ser Val Trp Cys Trp Ser
          20          25          30

cgc cca cac act gtg gca gag cag acc cac ctg ttg tca ctg gga aat      144
Arg Pro His Thr Val Ala Glu Gln Thr His Leu Leu Ser Leu Gly Asn
          35          40          45

gag ggg ctg cag gta ctg ccc tta gac aat gga gag gct tct gga ctg      192
Glu Gly Leu Gln Val Leu Pro Leu Asp Asn Gly Glu Ala Ser Gly Leu
          50          55          60

tca ctc caa ctt gga atc aaa tgg acc act gag aaa ccc gtg gaa gac      240

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Ser Leu Gln Leu Gly Ile Lys Trp Thr Thr Glu Lys Pro Val Glu Asp
65 70 75 80

agc agg tct aag gaa atc aca aag att aga aat gca tcc atg tgc acc 288
Ser Arg Ser Lys Glu Ile Thr Lys Ile Arg Asn Ala Ser Met Cys Thr
85 90 95

caa ctc cct cct agt gtg ggt ggg ggc acc tgc aat agt ctc tgg tac 336
Gln Leu Pro Pro Ser Val Gly Gly Gly Thr Cys Asn Ser Leu Trp Tyr
100 105 110

acg aga gtt gtt caa gaa ata gtc ctg cat gaa aga tca gaa gag aaa 384
Thr Arg Val Val Gln Glu Ile Val Leu His Glu Arg Ser Glu Glu Lys
115 120 125

tgg aga gac tcc cga agt ggg aag ttc aca ttt cag gac gtg aga aaa 432
Trp Arg Asp Ser Arg Ser Gly Lys Phe Thr Phe Gln Asp Val Arg Lys
130 135 140

cgc tga 438
Arg *
145

<210> 248
<211> 145
<212> PRT
<213> Homo sapiens

<400> 248

Met Ser Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Phe Lys Trp
1 5 10 15

Lys Arg Arg Val Val Ser Gly His Leu Leu Ser Val Trp Cys Trp Ser
20 25 30

Arg Pro His Thr Val Ala Glu Gln Thr His Leu Leu Ser Leu Gly Asn
35 40 45

Glu Gly Leu Gln Val Leu Pro Leu Asp Asn Gly Glu Ala Ser Gly Leu
50 55 60

Ser Leu Gln Leu Gly Ile Lys Trp Thr Thr Glu Lys Pro Val Glu Asp
65 70 75 80

Ser Arg Ser Lys Glu Ile Thr Lys Ile Arg Asn Ala Ser Met Cys Thr
85 90 95

Gln Leu Pro Pro Ser Val Gly Gly Gly Thr Cys Asn Ser Leu Trp Tyr

100 105 110
 Thr Arg Val Val Gln Glu Ile Val Leu His Glu Arg Ser Glu Glu Lys
 115 120 125
 Trp Arg Asp Ser Arg Ser Gly Lys Phe Thr Phe Gln Asp Val Arg Lys
 130 135 140
 Arg
 145

<210> 249
 <211> 552
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(552)

<400> 249
 atg aaa gtg gtg gtg gtg atg gtg gta ata ctg gtg gtg gtg aca ttg 48
 Met Lys Val Val Val Val Met Val Val Ile Leu Val Val Val Thr Leu
 1 5 10 15
 gtg gtg gtg gtg atg gtg gtg ata ctg gtg atg gtg gtg atg gtg gtg 96
 Val Val Val Val Met Val Val Ile Leu Val Met Val Val Met Val Val
 20 25 30
 gcg ctg gtg acc ctg aca tgg ggt cca gta gca gtg aca gtg gat gca 144
 Ala Leu Val Thr Leu Thr Trp Gly Pro Val Ala Val Thr Val Asp Ala
 35 40 45
 ggc tcc tgt ctc tca gca aac ctg ctg ggc gac agc gga ctc aga tgc 192
 Gly Ser Cys Leu Ser Ala Asn Leu Leu Gly Asp Ser Gly Leu Arg Cys
 50 55 60
 ctt ctg gaa tgt ctg ccg cag gtg ccc atc tcc ggt ttg ctt gac ctg 240
 Leu Leu Glu Cys Leu Pro Gln Val Pro Ile Ser Gly Leu Leu Asp Leu
 65 70 75 80
 ggc tct gag cag agc ttc cgg att cac ttc tcc aga gag gac cag gct 288
 Gly Ser Glu Gln Ser Phe Arg Ile His Phe Ser Arg Glu Asp Gln Ala
 85 90 95
 ggg aag aca ctc agg cta agt gag tgc agc ttc cgg cca gag cac gtg 336

Gly Lys Thr Leu Arg Leu Ser Glu Cys Ser Phe Arg Pro Glu His Val
 100 105 110

tcc agg ctg gcc acc ggc ttg agc aag tcc ctg cag ctg acg gag ctc 384
 Ser Arg Leu Ala Thr Gly Leu Ser Lys Ser Leu Gln Leu Thr Glu Leu
 115 120 125

acg ctg acc cag tgc tgc ctg ggc cag aag cag ctg gcc atc ctc ctg 432
 Thr Leu Thr Gln Cys Cys Leu Gly Gln Lys Gln Leu Ala Ile Leu Leu
 130 135 140

agc ttg gtg ggg cga ccc gca ggg ctg ttc agc ctc aga gac aac tgc 480
 Ser Leu Val Gly Arg Pro Ala Gly Leu Phe Ser Leu Arg Asp Asn Cys
 145 150 155 160

aga gct aca aag aca gca cat cca caa atg gag acc atc aca tca tcg 528
 Arg Ala Thr Lys Thr Ala His Pro Gln Met Glu Thr Ile Thr Ser Ser
 165 170 175

aca ata gca gct tct gtt tac taa 552
 Thr Ile Ala Ala Ser Val Tyr *

<210> 250

<211> 183

<212> PRT

<213> Homo sapiens

<400> 250

Met Lys Val Val Val Val Met Val Val Ile Leu Val Val Val Thr Leu
 1 5 10 15

Val Val Val Val Met Val Val Ile Leu Val Met Val Val Met Val Val
 20 25 30

Ala Leu Val Thr Leu Thr Trp Gly Pro Val Ala Val Thr Val Asp Ala
 35 40 45

Gly Ser Cys Leu Ser Ala Asn Leu Leu Gly Asp Ser Gly Leu Arg Cys
 50 55 60

Leu Leu Glu Cys Leu Pro Gln Val Pro Ile Ser Gly Leu Leu Asp Leu
 65 70 75 80

Gly Ser Glu Gln Ser Phe Arg Ile His Phe Ser Arg Glu Asp Gln Ala
 85 90 95

Gly Lys Thr Leu Arg Leu Ser Glu Cys Ser Phe Arg Pro Glu His Val


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<210> 251
<211> 546
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (1)...(546)

<400> 251																
atg	aaa	aca	ttg	gat	cgg	aag	gtt	ttc	ttc	ctg	tct	tca	ctg	ctc	att	48
Met	Lys	Thr	Leu	Asp	Arg	Lys	Val	Phe	Phe	Leu	Ser	Ser	Leu	Leu	Ile	
1			5			10			15							
gga	ctt	tca	gga	ctg	gaa	gag	ccc	ctc	tac	ctt	aaa	ttt	aga	gtt	aca	96
Gly	Leu	Ser	Gly	Leu	Glu	Glu	Pro	Leu	Tyr	Leu	Lys	Phe	Arg	Val	Thr	
20			25			30										
ggt	tca	ttg	gaa	aga	gca	tca	acc	caa	cct	gct	tac	atc	aga	gac	ctg	144
Gly	Ser	Leu	Glu	Arg	Ala	Ser	Thr	Gln	Pro	Ala	Tyr	Ile	Arg	Asp	Leu	
35			40			45										
aac	act	cag	tgt	gac	tgt	gcg	aac	tcc	ccg	tac	agg	aca	ttt	att	aat	192
Asn	Thr	Gln	Cys	Asp	Cys	Ala	Asn	Ser	Pro	Tyr	Arg	Thr	Phe	Ile	Asn	
50			55			60										
gct	agt	atg	cac	ttt	ctc	cct	ctt	agt	aat	aac	att	cca	gag	tcc	tct	240
Ala	Ser	Met	His	Phe	Leu	Pro	Leu	Ser	Asn	Asn	Ile	Pro	Glu	Ser	Ser	
65			70			75			80							
tgg	gga	gaa	atc	tcc	att	gac	ttt	gtg	gaa	ctg	caa	ggc	aag	gtg	cct	288

Trp Gly Glu Ile Ser Ile Asp Phe Val Glu Leu Gln Gly Lys Val Pro
 85 90 95

 agt tct cca atc acc aag atg tgc aca cat gac cca ttg gcc aag tgg 336
 Ser Ser Pro Ile Thr Lys Met Cys Thr His Asp Pro Leu Ala Lys Trp
 100 105 110

 aca ctc tct ccc aaa tct tcg aat ctc aag cag atg gat gca agg atg 384
 Thr Leu Ser Pro Lys Ser Ser Asn Leu Lys Gln Met Asp Ala Arg Met
 115 120 125

 gaa aac agc tgg aat cga ctc att tca gtg gga tca gaa agg gca gcc 432
 Glu Asn Ser Trp Asn Arg Leu Ile Ser Val Gly Ser Glu Arg Ala Ala
 130 135 140

 aca gag tta ggt gag aag gca cag ctg aag cga tgg aag att tac atc 480
 Thr Glu Leu Gly Glu Lys Ala Gln Leu Lys Arg Trp Lys Ile Tyr Ile
 145 150 155 160

 ata tct gtc agc atg tca ata acc cat cct gaa att cag gaa agg ctg 528
 Ile Ser Val Ser Met Ser Ile Thr His Pro Glu Ile Gln Glu Arg Leu
 165 170 175

 aaa aac tgt cta act tga 546
 Lys Asn Cys Leu Thr *
 180

<210> 252
 <211> 181
 <212> PRT
 <213> Homo sapiens

<400> 252
 Met Lys Thr Leu Asp Arg Lys Val Phe Phe Leu Ser Ser Leu Leu Ile
 1 5 10 15
 Gly Leu Ser Gly Leu Glu Glu Pro Leu Tyr Leu Lys Phe Arg Val Thr
 20 25 30
 Gly Ser Leu Glu Arg Ala Ser Thr Gln Pro Ala Tyr Ile Arg Asp Leu
 35 40 45
 Asn Thr Gln Cys Asp Cys Ala Asn Ser Pro Tyr Arg Thr Phe Ile Asn
 50 55 60
 Ala Ser Met His Phe Leu Pro Leu Ser Asn Asn Ile Pro Glu Ser Ser

Gln Pro Leu Gly Ser Glu Gln Gln Gly Pro Phe Ile Ser Val Arg Cys
65 70 75 80

tgg gct cgg gac ctg cag ccc gcc atg cct gag ctt ccc acc cac tcc 288
Trp Ala Arg Asp Leu Gln Pro Ala Met Pro Glu Leu Pro Thr His Ser
85 90 95

atg ggc tcc tgt gcg gcc cga gcc tcc ccg acg agc gcc acc ccc tgc 336
Met Gly Ser Cys Ala Ala Arg Ala Ser Pro Thr Ser Ala Thr Pro Cys
100 105 110

tcc acg gcg ccc agt ccc atc gac cac cca agg gct gag gag tgc gag 384
Ser Thr Ala Pro Ser Pro Ile Asp His Pro Arg Ala Glu Glu Cys Glu
115 120 125

cgc acg gcg cgg gac tgg cag cct gca gat ggc cta ctg tga 426
Arg Thr Ala Arg Asp Trp Gln Pro Ala Asp Gly Leu Leu *
130 135 140

<210> 254
<211> 141
<212> PRT
<213> Homo sapiens

<400> 254
Met Arg Pro Arg Lys Ala Phe Leu Leu Leu Leu Leu Gly Leu Val
1 5 10 15
Gln Leu Leu Ala Val Ala Gly Ala Glu Gly Pro Asp Glu Gly Leu Pro
20 25 30
Leu Ser Ser Gly Ile Cys Phe Leu Asn Tyr Asn Pro Ala Ser Ser Thr
35 40 45
Ala Tyr Phe Leu Asp Ile Val Val Gln Pro Leu Gly Lys Gln Leu Glu
50 55 60
Gln Pro Leu Gly Ser Glu Gln Gln Gly Pro Phe Ile Ser Val Arg Cys
65 70 75 80
Trp Ala Arg Asp Leu Gln Pro Ala Met Pro Glu Leu Pro Thr His Ser
85 90 95
Met Gly Ser Cys Ala Ala Arg Ala Ser Pro Thr Ser Ala Thr Pro Cys
100 105 110
Ser Thr Ala Pro Ser Pro Ile Asp His Pro Arg Ala Glu Glu Cys Glu
115 120 125
Arg Thr Ala Arg Asp Trp Gln Pro Ala Asp Gly Leu Leu

gag tat aca tat gct tgc tat ata aac tgc act gcc tct gcc gga att	432
Glu Tyr Thr Tyr Ala Cys Tyr Ile Asn Cys Thr Ala Ser Ala Gly Ile	
130 135 140	
gtc acc gag atg ctc agg cct ttc atc act ctt gtg tct aga gcc gcc	480
Val Thr Glu Met Leu Arg Pro Phe Ile Thr Leu Val Ser Arg Ala Ala	
145 150 155 160	
agg tgg tcc cag gac ccc ttt tca cct agc agt tcc gca gcc cat cgg	528
Arg Trp Ser Gln Asp Pro Phe Ser Pro Ser Ser Ser Ala Ala His Arg	
165 170 175	
caa tcc aca ccc cag atc cat ccc tgt atc gtg agc caa cct tcc tgc	576
Gln Ser Thr Pro Gln Ile His Pro Cys Ile Val Ser Gln Pro Ser Cys	
180 185 190	
aaa gtc ctc gtg ggc atc ggc atg tcc tat ttc tct ttc ctt ggg gca	624
Lys Val Leu Val Gly Ile Gly Met Ser Tyr Phe Ser Phe Leu Gly Ala	
195 200 205	
tcc tcg tca tta atg acc cca tcc gcg aca atc cta ccg ctg ctg tcc	672
Ser Ser Ser Leu Met Thr Pro Ser Ala Thr Ile Leu Pro Leu Leu Ser	
210 215 220	
tgc cgt gcg tct ctg acg gtg agc tta gtc agt cgt ctt cgc agt aga	720
Cys Arg Ala Ser Leu Thr Val Ser Leu Val Ser Arg Leu Arg Ser Arg	
225 230 235 240	
cac agc tcc cgg ata gct gct acc aag ttc gac gca tct ata tat cgc	768
His Ser Ser Arg Ile Ala Ala Thr Lys Phe Asp Ala Ser Ile Tyr Arg	
245 250 255	
tgc gcg tca gac gcc ggc gac aca cgc atc ttc cgt agt cat gcc ggg	816
Cys Ala Ser Asp Ala Gly Asp Thr Arg Ile Phe Arg Ser His Ala Gly	
260 265 270	
aga cgt cag ccg agc agt aca tat cgc gtt gta ccg aca atc cta agt	864
Arg Arg Gln Pro Ser Ser Thr Tyr Arg Val Val Pro Thr Ile Leu Ser	
275 280 285	
gca atc gat gtg gtt gtc gca agc tcc gtc aca agc tgc cgc gtc ttc	912
Ala Ile Asp Val Val Val Ala Ser Ser Val Thr Ser Cys Arg Val Phe	

290

295

300

gtg gct aac agc ggc gca tgt gcg ccc tga
 Val Ala Asn Ser Gly Ala Cys Ala Pro *
 305 310

942

<210> 256

<211> 313

<212> PRT

<213> Homo sapiens

<400> 256

Met Glu Asp Tyr Ile His Lys Leu Val Tyr Thr Val Phe Ala Cys Gly
 1 5 10 15
 Arg His Pro Ala Leu Leu Leu Leu Phe Val Pro Val Leu Pro Ser Ala
 20 25 30
 Gly Ser Ser Pro Leu Pro Gly His Val Leu Ser Ile Phe Ser Pro Pro
 35 40 45
 Ala Arg Ile Pro His Ala Arg Ser Val Ser Ser Gln Leu Phe Pro Tyr
 50 55 60
 Ala Ala Val Ala Ser Phe Gly Pro Ser Leu Arg Val Val Glu Phe Leu
 65 70 75 80
 Glu Arg Leu Leu Leu Val Arg Ala Ala Asp Arg Ser Cys Arg Ser Arg
 85 90 95
 Phe Ala Pro Ile Arg Asp Arg Gly Leu Arg Ser Ser Arg Cys Arg Thr
 100 105 110
 Asp Leu Arg Val Ser Gly Trp His Gly Leu Pro Leu Asp Leu Pro Lys
 115 120 125
 Glu Tyr Thr Tyr Ala Cys Tyr Ile Asn Cys Thr Ala Ser Ala Gly Ile
 130 135 140
 Val Thr Glu Met Leu Arg Pro Phe Ile Thr Leu Val Ser Arg Ala Ala
 145 150 155 160
 Arg Trp Ser Gln Asp Pro Phe Ser Pro Ser Ser Ser Ala Ala His Arg
 165 170 175
 Gln Ser Thr Pro Gln Ile His Pro Cys Ile Val Ser Gln Pro Ser Cys
 180 185 190
 Lys Val Leu Val Gly Ile Gly Met Ser Tyr Phe Ser Phe Leu Gly Ala
 195 200 205
 Ser Ser Ser Leu Met Thr Pro Ser Ala Thr Ile Leu Pro Leu Leu Ser
 210 215 220
 Cys Arg Ala Ser Leu Thr Val Ser Leu Val Ser Arg Leu Arg Ser Arg
 225 230 235 240

T002290.1.e258a

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<210> 257
<211> 291
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(291)
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<400> 257																
atg	ctt	tgg	ctc	ctt	ttg	gct	ctt	ttt	gcc	ccg	ggt	cgg	gcg	ggg	ggc	48
Met	Leu	Trp	Leu	Leu	Leu	Ala	Leu	Phe	Ala	Pro	Gly	Arg	Ala	Gly	Gly	
1			5			10			15							
ggg	ggg	tgg	ggg	tgc	atc	ttc	cct	gat	aca	cca	cac	tct	cca	ttc	cct	96
Gly	Gly	Trp	Gly	Cys	Ile	Phe	Pro	Asp	Thr	Pro	His	Ser	Pro	Phe	Pro	
			20			25						30				
ggg	ata	tat	gac	act	gat	tgg	gct	acc	acg	atc	ggg	gac	tcc	aca	cca	144
Gly	Ile	Tyr	Asp	Thr	Asp	Trp	Ala	Thr	Thr	Ile	Gly	Asp	Ser	Thr	Pro	
35						40						45				
cta	cta	tgg	ccc	ttc	att	tct	gtg	gct	ctg	tgc	tcc	tcc	agt	gca	ctt	192
Leu	Leu	Trp	Pro	Phe	Ile	Ser	Val	Ala	Leu	Cys	Ser	Ser	Ser	Ala	Leu	
50						55						60				
cct	gca	ggg	cac	ccg	gca	ttc	ccc	aat	cct	aga	cgc	tac	gca	gat	gcc	240
Pro	Ala	Gly	His	Pro	Ala	Phe	Pro	Asn	Pro	Arg	Arg	Tyr	Ala	Asp	Ala	
65						70			75			80				
agc	cat	gca	gaa	tca	cat	acc	atc	tta	cct	gct	gag	ctc	tcc	cct	ttg	288
Ser	His	Ala	Glu	Ser	His	Thr	Ile	Leu	Pro	Ala	Glu	Leu	Ser	Pro	Leu	

260

85

90

95

tga
*

291

<210> 258

<211> 96

<212> PRT

<213> Homo sapiens

<400> 258

Met Leu Trp Leu Leu Leu Ala Leu Phe Ala Pro Gly Arg Ala Gly Gly
1 5 10 15
Gly Gly Trp Gly Cys Ile Phe Pro Asp Thr Pro His Ser Pro Phe Pro
20 25 30
Gly Ile Tyr Asp Thr Asp Trp Ala Thr Thr Ile Gly Asp Ser Thr Pro
35 40 45
Leu Leu Trp Pro Phe Ile Ser Val Ala Leu Cys Ser Ser Ser Ala Leu
50 55 60
Pro Ala Gly His Pro Ala Phe Pro Asn Pro Arg Arg Tyr Ala Asp Ala
65 70 75 80
Ser His Ala Glu Ser His Thr Ile Leu Pro Ala Glu Leu Ser Pro Leu
85 90 95

<210> 259

<211> 231

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(231)

<400> 259

atg aaa ctc atg gaa aca ctt aac cag tgc ata aac gct ggt cat gaa 48
Met Lys Leu Met Glu Thr Leu Asn Gln Cys Ile Asn Ala Gly His Glu
1 5 10 15

atg acg aag gct atc gcc att gca cag ttt aat gat gac agc ccg gaa 96
Met Thr Lys Ala Ile Ala Ile Ala Gln Phe Asn Asp Asp Ser Pro Glu
20 25 30


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<210> 262
<211> 124
<212> PRT
<213> Homo sapiens

      <400> 262
Met Lys Phe Leu Leu Leu Val Leu Ala Ala Leu Gly Phe Leu Thr Gln
 1             5             10             15
Val Ile Pro Gly Ala Asp Ser Ala Val Lys Cys Ala Pro Gly Asp Ser
      20             25             30
Arg Pro Gly Arg Ile Pro His Arg Ser Pro Thr Pro Arg Ser Pro Pro
      35             40             45

```

Ser Arg Leu Ile Asp Leu Cys Gln Ser Leu Pro Pro Ser Ala Gly Ser
 50 55 60
 Thr Arg Tyr Thr Arg Ala Leu Glu Val Ala Arg Ala Gly Gln Thr Gly
 65 70 75 80
 Ala Pro Asp Thr Phe Gln Gly Pro Ala Lys Asp Leu Pro Met Ser Thr
 85 90 95
 Gly Val Pro Asp Thr Arg Asp Pro Gly Gln Asp Ser His Phe Thr Arg
 100 105 110
 Tyr Thr Asp Thr Gly Leu Arg Glu Gln Glu Ile Pro
 115 120

<210> 263
 <211> 420
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(420)

<400> 263

atg aaa gag gca ttg acc aac cag aca cca atg act caa caa ctt gat 48
 Met Lys Glu Ala Leu Thr Asn Gln Thr Pro Met Thr Gln Gln Leu Asp
 1 5 10 15

att agc ctg att tta ctg atg gcc act tgg gaa ctg gtg caa gga gtg 96
 Ile Ser Leu Ile Leu Leu Met Ala Thr Trp Glu Leu Val Gln Gly Val
 20 25 30

cag agg att cga gta tca ctt att gtt ctt cct gat gac cca ctg gag 144
 Gln Arg Ile Arg Val Ser Leu Ile Val Leu Pro Asp Asp Pro Leu Glu
 35 40 45

gac ttg cgc ttc tat tct tac aca ttt gtg tcc ttt gga gtt aga gtt 192
 Asp Leu Arg Phe Tyr Ser Tyr Thr Phe Val Ser Phe Gly Val Arg Val
 50 55 60

cat ggt tct act ctt gcc ata cga cac att aaa ata caa gct atg gct 240
 His Gly Ser Thr Leu Ala Ile Arg His Ile Lys Ile Gln Ala Met Ala
 65 70 75 80

gct gct ggc cac ttt gaa ttc cat ctt ggc aga gaa gtc cgt gaa ggt 288
 Ala Ala Gly His Phe Glu Phe His Leu Gly Arg Glu Val Arg Glu Gly

	85	90	95	
cac tta gaa gtt att ttc caa aca tgc aat gga aag tgt atc tct gtg				336
His Leu Glu Val Ile Phe Gln Thr Cys Asn Gly Lys Cys Ile Ser Val				
	100	105	110	
act aaa caa gtg gac tgt ggt ggc cat agt aga gca cga ctc aga ttg				384
Thr Lys Gln Val Asp Cys Gly Gly His Ser Arg Ala Arg Leu Arg Leu				
	115	120	125	
tcc tct gaa aaa acc tgc tgt aga aag cat att tga				420
Ser Ser Glu Lys Thr Cys Cys Arg Lys His Ile *				
	130	135		

<210> 264
 <211> 139
 <212> PRT
 <213> Homo sapiens

<400> 264

Met Lys Glu Ala Leu Thr Asn Gln Thr Pro Met Thr Gln Gln Leu Asp				
1	5	10	15	
Ile Ser Leu Ile Leu Leu Met Ala Thr Trp Glu Leu Val Gln Gly Val				
	20	25	30	
Gln Arg Ile Arg Val Ser Leu Ile Val Leu Pro Asp Asp Pro Leu Glu				
	35	40	45	
Asp Leu Arg Phe Tyr Ser Tyr Thr Phe Val Ser Phe Gly Val Arg Val				
50	55	60		
His Gly Ser Thr Leu Ala Ile Arg His Ile Lys Ile Gln Ala Met Ala				
65	70	75	80	
Ala Ala Gly His Phe Glu Phe His Leu Gly Arg Glu Val Arg Glu Gly				
	85	90	95	
His Leu Glu Val Ile Phe Gln Thr Cys Asn Gly Lys Cys Ile Ser Val				
	100	105	110	
Thr Lys Gln Val Asp Cys Gly Gly His Ser Arg Ala Arg Leu Arg Leu				
	115	120	125	
Ser Ser Glu Lys Thr Cys Cys Arg Lys His Ile				
130	135			

<210> 265
 <211> 477
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(477)

<400> 265

atg ttt tat tgg ttg gtg caa cgg gta gcc tgt gtt tta ctg tta act	48
Met Phe Tyr Trp Leu Val Gln Arg Val Ala Cys Val Leu Leu Leu Thr	
1 5 10 15	
gca atg ctt ttt caa acg gat gct ttt gaa aca ccc tgg aat ata gtt	96
Ala Met Leu Phe Gln Thr Asp Ala Phe Glu Thr Pro Trp Asn Ile Val	
20 25 30	
ggc aga atg aat aaa gga atg aat aaa agc att gtt cac ata atg cga	144
Gly Arg Met Asn Lys Gly Met Asn Lys Ser Ile Val His Ile Met Arg	
35 40 45	
tat aac ttt cta gaa ggt caa att aac cct act ttc gat gta gaa atg	192
Tyr Asn Phe Leu Glu Gly Gln Ile Asn Pro Thr Phe Asp Val Glu Met	
50 55 60	
act aac ata acc gaa gat cta atg gtg atg tgg tca tgc aca cag tgt	240
Thr Asn Ile Thr Glu Asp Leu Met Val Met Trp Ser Cys Thr Gln Cys	
65 70 75 80	
gta ggt gct acc aac tgt tgc aga cac agt tca tct cag aac aga aag	288
Val Gly Ala Thr Asn Cys Cys Arg His Ser Ser Ser Gln Asn Arg Lys	
85 90 95	
cat gaa act cta gcc aca gga atc aga atc ctt ctt ccc caa ggg tca	336
His Glu Thr Leu Ala Thr Gly Ile Arg Ile Leu Leu Pro Gln Gly Ser	
100 105 110	
atc act cat tcc cca gct gct gaa agt gtg gct gcc aat tgt tta cag	384
Ile Thr His Ser Pro Ala Ala Glu Ser Val Ala Ala Asn Cys Leu Gln	
115 120 125	
ctg tat cct tct ctc aag cat tac tct cag tct ctg gga gcc aag tct	432
Leu Tyr Pro Ser Leu Lys His Tyr Ser Gln Ser Leu Gly Ala Lys Ser	
130 135 140	

477

<400> 266

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<220>  
<221> CDS  
<222> (1)...(603)
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48

Met	Ala	Ala	Ala	Trp	Thr	Val	Val	Leu	Val	Thr	Leu	Val	Leu	Gly	Leu	
1				5				10						15		
gcc	gtg	gca	ggc	cct	gtc	ccc	act	tcc	aag	ccc	acc	aca	act	ggg	aag	96
Ala	Val	Ala	Gly	Pro	Val	Pro	Thr	Ser	Lys	Pro	Thr	Thr	Thr	Gly	Lys	
			20					25						30		
ggc	tgc	cac	att	ggc	agg	ttc	aaa	tct	ctg	tca	cca	cag	gag	cta	gcg	144
Gly	Cys	His	Ile	Gly	Arg	Phe	Lys	Ser	Leu	Ser	Pro	Gln	Glu	Leu	Ala	
		35					40						45			
agc	ttc	aag	aag	gcc	agg	gac	gcc	ttg	gaa	gag	tca	ctc	aag	ctg	aaa	192
Ser	Phe	Lys	Lys	Ala	Arg	Asp	Ala	Leu	Glu	Glu	Ser	Leu	Lys	Leu	Lys	
	50					55					60					
aac	tgg	agt	tgc	agc	tct	cct	gtc	ttc	ccc	ggg	aat	tgg	gac	ctg	agg	240
Asn	Trp	Ser	Cys	Ser	Ser	Pro	Val	Phe	Pro	Gly	Asn	Trp	Asp	Leu	Arg	
65					70				75					80		
ctt	ctc	cag	gtg	agg	gag	cgc	cct	gtg	gcc	ttg	gag	gct	gag	ctg	gcc	288
Leu	Leu	Gln	Val	Arg	Glu	Arg	Pro	Val	Ala	Leu	Glu	Ala	Glu	Leu	Ala	
				85					90					95		
ctg	acg	ctg	aag	gtc	ctg	gag	gcc	gct	gct	ggc	cca	gcc	ctg	gag	gac	336
Leu	Thr	Leu	Lys	Val	Leu	Glu	Ala	Ala	Ala	Gly	Pro	Ala	Leu	Glu	Asp	
			100				105						110			
gtc	cta	gac	cag	ccc	ctt	cac	acc	ctg	cac	cac	atc	ctc	tcc	cag	ctc	384
Val	Leu	Asp	Gln	Pro	Leu	His	Thr	Leu	His	His	Ile	Leu	Ser	Gln	Leu	
		115					120					125				
cag	gcc	tgt	atc	cag	cct	cag	ccc	aca	gca	ggg	ccc	agg	ccc	cgg	ggc	432
Gln	Ala	Cys	Ile	Gln	Pro	Gln	Pro	Thr	Ala	Gly	Pro	Arg	Pro	Arg	Gly	
	130					135					140					
cgc	ctc	cac	cac	tgg	ctg	cac	cgg	ctc	cag	gag	gcc	ccc	aaa	aag	gag	480
Arg	Leu	His	His	Trp	Leu	His	Arg	Leu	Gln	Glu	Ala	Pro	Lys	Lys	Glu	
145					150					155					160	
tcc	gct	ggc	tgc	ctg	gag	gca	tct	gtc	acc	ttc	aac	ctc	ttc	cgc	ctc	528
Ser	Ala	Gly	Cys	Leu	Glu	Ala	Ser	Val	Thr	Phe	Asn	Leu	Phe	Arg	Leu	
				165					170					175		

ctc acg cga gac ctc aaa tat gtg gcc gat ggg gac ctg tgt ctg aga 576
 Leu Thr Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg
 180 185 190

acg tca acc cac cct gag tcc acc tga 603
 Thr Ser Thr His Pro Glu Ser Thr *
 195 200

<210> 268

<211> 200

<212> PRT

<213> Homo sapiens

<400> 268

Met Ala Ala Ala Trp Thr Val Val Leu Val Thr Leu Val Leu Gly Leu
 1 5 10 15
 Ala Val Ala Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys
 20 25 30
 Gly Cys His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala
 35 40 45
 Ser Phe Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys
 50 55 60
 Asn Trp Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg
 65 70 75 80
 Leu Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala
 85 90 95
 Leu Thr Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp
 100 105 110
 Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu
 115 120 125
 Gln Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly
 130 135 140
 Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu
 145 150 155 160
 Ser Ala Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu
 165 170 175
 Leu Thr Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg
 180 185 190
 Thr Ser Thr His Pro Glu Ser Thr
 195 200

<210> 269

<211> 624
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(624)

<400> 269

atg gga aga atc ccg gta att ctg ctg ctg gct gcc ccc cct gtc tcc	48
Met Gly Arg Ile Pro Val Ile Leu Leu Leu Ala Ala Pro Pro Val Ser	
1 5 10 15	

ctg tca gcg gtg cga cta gct act agt agt agg agg act aag cca cta	96
Leu Ser Ala Val Arg Leu Ala Thr Ser Ser Arg Arg Thr Lys Pro Leu	
20 25 30	

acg agc ttc ctc gct ctg cag aaa cgt ttg ggc ctc gtc cca tcg gcg	144
Thr Ser Phe Leu Ala Leu Gln Lys Arg Leu Gly Leu Val Pro Ser Ala	
35 40 45	

gac tat atg cag tat ctc cct att gta cgt cgg ggc agg cag cat agc	192
Asp Tyr Met Gln Tyr Leu Pro Ile Val Arg Arg Gly Arg Gln His Ser	
50 55 60	

att gtg gcg tcc acc cag acg ggc cgg gct tcg gta gtg act gct act	240
Ile Val Ala Ser Thr Gln Thr Gly Arg Ala Ser Val Val Thr Ala Thr	
65 70 75 80	

tac tct ggc gcg cgc gat atc tca ggc atc agt ttt cga acc agg gct	288
Tyr Ser Gly Ala Arg Asp Ile Ser Gly Ile Ser Phe Arg Thr Arg Ala	
85 90 95	

cat aga gcc ctc gga tat tta ctt cac aga gtt ttt atg agg ata gct	336
His Arg Ala Leu Gly Tyr Leu Leu His Arg Val Phe Met Arg Ile Ala	
100 105 110	

ttt gat aga agc tgc agg agc ctg cgc gtc atc cga gat gcc cac ggg	384
Phe Asp Arg Ser Cys Arg Ser Leu Arg Val Ile Arg Asp Ala His Gly	
115 120 125	

ggt ctt cct tac ctt cag gtg gaa tgc cac ccc agg gac aac cct cct	432
Gly Leu Pro Tyr Leu Gln Val Glu Cys His Pro Arg Asp Asn Pro Pro	

130

135

140

gtg gag tac ttg ttc cta cac ctt ggt tgg cga gag caa acc gat gca 480
 Val Glu Tyr Leu Phe Leu His Leu Gly Trp Arg Glu Gln Thr Asp Ala
 145 150 155 160

ggc gtt tct aaa aca aat gag ccc tgg gag agc cct gaa cgc att tat 528
 Gly Val Ser Lys Thr Asn Glu Pro Trp Glu Ser Pro Glu Arg Ile Tyr
 165 170 175

tat gag cct cga ggg act ggg aag ctg cag aga ccc aaa gct gtc cga 576
 Tyr Glu Pro Arg Gly Thr Gly Lys Leu Gln Arg Pro Lys Ala Val Arg
 180 185 190

gag gac ttg gga ctt gct ctg caa aag acc tgg cct ctg ctt ttt tga 624
 Glu Asp Leu Gly Leu Ala Leu Gln Lys Thr Trp Pro Leu Leu Phe *
 195 200 205

<210> 270

<211> 207

<212> PRT

<213> Homo sapiens

<400> 270

Met Gly Arg Ile Pro Val Ile Leu Leu Leu Ala Ala Pro Pro Val Ser
 1 5 10 15
 Leu Ser Ala Val Arg Leu Ala Thr Ser Ser Arg Arg Thr Lys Pro Leu
 20 25 30
 Thr Ser Phe Leu Ala Leu Gln Lys Arg Leu Gly Leu Val Pro Ser Ala
 35 40 45
 Asp Tyr Met Gln Tyr Leu Pro Ile Val Arg Arg Gly Arg Gln His Ser
 50 55 60
 Ile Val Ala Ser Thr Gln Thr Gly Arg Ala Ser Val Val Thr Ala Thr
 65 70 75 80
 Tyr Ser Gly Ala Arg Asp Ile Ser Gly Ile Ser Phe Arg Thr Arg Ala
 85 90 95
 His Arg Ala Leu Gly Tyr Leu Leu His Arg Val Phe Met Arg Ile Ala
 100 105 110
 Phe Asp Arg Ser Cys Arg Ser Leu Arg Val Ile Arg Asp Ala His Gly
 115 120 125
 Gly Leu Pro Tyr Leu Gln Val Glu Cys His Pro Arg Asp Asn Pro Pro
 130 135 140

210	215	220
Ile Leu Leu Trp Leu Val Thr Val Met Asp Ala Leu Leu Ile Arg Gly		
225	230	235
Val Ser Leu Ser Asn Asp Tyr Leu Ile Leu Phe Ser Ile Asp Thr Arg		240
	245	250
Thr Arg Ala Arg Leu Arg Met Asp Arg Leu Ser Ala Ser Val Ser Met		255
	260	265
Leu Thr Asp Thr Ala Met Val Leu Val Thr Asp Ile Val Met Arg Ala		270
	275	280
Val Leu Val Thr Leu His Ala		285
290	295	

<210> 273
 <211> 579
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(579)

<400> 273

atg ctt ctg att gag ctg ggc ttg gct gat cga gtc tgg gct cgc tca	48
Met Leu Leu Ile Glu Leu Gly Leu Ala Asp Arg Val Trp Ala Arg Ser	
1 5 10 15	

tgt gtc tgt ggg ctg ccg gca gct cag caa ggg gct ggc tgg act agc	96
Cys Val Cys Gly Leu Pro Ala Ala Gln Gln Gly Ala Gly Trp Thr Ser	
20 25 30	

gaa gcc atg aag cca cga agc cac ggg ctt gtc aca ggc ttt cag ggg	144
Glu Ala Met Lys Pro Arg Ser His Gly Leu Val Thr Gly Phe Gln Gly	
35 40 45	

aca cag caa aca gta aaa gct ctg cag att caa cga agg cca gct ggg	192
Thr Gln Gln Thr Val Lys Ala Leu Gln Ile Gln Arg Arg Pro Ala Gly	
50 55 60	

ttt gaa cca gcc atg cag ggg aac ctc cag ggt tcc ctt cga att gga	240
Phe Glu Pro Ala Met Gln Gly Asn Leu Gln Gly Ser Leu Arg Ile Gly	
65 70 75 80	

cat tgc cat tgt ccc ctg ggt gca gat gag ggc agt gac ctg cct gag	288
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<210> 275
<211> 510
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(510)
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<400> 275																
atg	agg	tca	gaa	gcc	ttg	ctg	cta	tat	ttc	aca	ctg	cta	cac	ttt	gct	48
Met	Arg	Ser	Glu	Ala	Leu	Leu	Leu	Tyr	Phe	Thr	Leu	Leu	His	Phe	Ala	
1			5			10			15							
ggg	gct	ggt	ttc	cca	gaa	gat	tct	gag	cca	atc	agt	att	tcg	cat	ggc	96
Gly	Ala	Gly	Phe	Pro	Glu	Asp	Ser	Glu	Pro	Ile	Ser	Ile	Ser	His	Gly	
			20			25			30							
aac	tat	aca	aaa	cag	tat	ccg	gtg	ttt	gtg	ggc	cac	aag	cca	gga	cgg	144
Asn	Tyr	Thr	Lys	Gln	Tyr	Pro	Val	Phe	Val	Gly	His	Lys	Pro	Gly	Arg	
			35			40			45							
aac	acc	aca	cag	agg	cac	agg	ctg	gac	atc	cag	atg	att	atg	atc	atg	192

35 40 45
 Asn Thr Thr Gln Arg His Arg Leu Asp Ile Gln Met Ile Met Ile Met
 50 55 60
 Asn Gly Thr Leu Tyr Ile Ala Ala Arg Thr Gln Arg Gly Phe Val Val
 65 70 75 80
 Phe Val Val Thr Gly Ser Thr Leu His Arg Cys Leu Leu Ile Thr Ser
 85 90 95
 Leu Trp Arg Gln Thr His Pro Ser Tyr His Ser Ser Ser Glu Thr Gly
 100 105 110
 Arg Pro Val Lys Gly Gly Glu Arg Gly Lys Cys Thr Leu Asn His Phe
 115 120 125
 Glu Leu Gly Tyr Trp Leu Pro Val Ser Tyr Thr Leu Arg Val Val Ile
 130 135 140
 Gly Val Gly Thr Leu Glu Tyr Ala Tyr Ser Ser Ser Lys Lys Lys Gln
 145 150 155 160
 Ser Trp His Tyr Cys Glu Lys Ser Thr
 165

<210> 277

<211> 423

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(423)

<400> 277

atg tcc acc acc aca tgc caa gtg gtg gcg ttc ctc ctg tcc atc ctg 48
 Met Ser Thr Thr Thr Cys Gln Val Val Ala Phe Leu Leu Ser Ile Leu
 1 5 10 15

ggg ctg gcc ggc tgc atc gcg gcc acc ggg atg gac atg tgg agc acc 96
 Gly Leu Ala Gly Cys Ile Ala Ala Thr Gly Met Asp Met Trp Ser Thr
 20 25 30

cag gac ctg tac gac aac ccc gtc acc tcc gtg ttc cag tac gaa ggg 144
 Gln Asp Leu Tyr Asp Asn Pro Val Thr Ser Val Phe Gln Tyr Glu Gly
 35 40 45

ctc tgg agg agc tgc gtg agg cag agt tca ggc ttc acc gaa tgc agg 192
 Leu Trp Arg Ser Cys Val Arg Gln Ser Ser Gly Phe Thr Glu Cys Arg
 50 55 60

ccc tat ttc acc atc ctg gga ctt cca gtc tct tac tcc ccc atc ctg 240
 Pro Tyr Phe Thr Ile Leu Gly Leu Pro Val Ser Tyr Ser Pro Ile Leu
 65 70 75 80

ttt ctt ctg tcc ttt cag tat acc ttg gac ttg gtc ctg gac atc cat 288
 Phe Leu Leu Ser Phe Gln Tyr Thr Leu Asp Leu Val Leu Asp Ile His
 85 90 95

tgc tcc tgc tcc cct gaa ttc ccc cct cca cca ccc caa ctg tcc tct 336
 Cys Ser Cys Ser Pro Glu Phe Pro Pro Pro Pro Gln Leu Ser Ser
 100 105 110

cac aaa tct tcc tcc aaa cct cct caa gcc ccc aaa ttg aat aaa gat 384
 His Lys Ser Ser Ser Lys Pro Pro Gln Ala Pro Lys Leu Asn Lys Asp
 115 120 125

tcc aca agt ctc tgt acc aaa ccc aga gca ttc tca tag 423
 Ser Thr Ser Leu Cys Thr Lys Pro Arg Ala Phe Ser *
 130 135 140

<210> 278

<211> 140

<212> PRT

<213> Homo sapiens

<400> 278

Met Ser Thr Thr Thr Cys Gln Val Val Ala Phe Leu Leu Ser Ile Leu
 1 5 10 15
 Gly Leu Ala Gly Cys Ile Ala Ala Thr Gly Met Asp Met Trp Ser Thr
 20 25 30
 Gln Asp Leu Tyr Asp Asn Pro Val Thr Ser Val Phe Gln Tyr Glu Gly
 35 40 45
 Leu Trp Arg Ser Cys Val Arg Gln Ser Ser Gly Phe Thr Glu Cys Arg
 50 55 60
 Pro Tyr Phe Thr Ile Leu Gly Leu Pro Val Ser Tyr Ser Pro Ile Leu
 65 70 75 80
 Phe Leu Leu Ser Phe Gln Tyr Thr Leu Asp Leu Val Leu Asp Ile His
 85 90 95
 Cys Ser Cys Ser Pro Glu Phe Pro Pro Pro Pro Gln Leu Ser Ser
 100 105 110
 His Lys Ser Ser Ser Lys Pro Pro Gln Ala Pro Lys Leu Asn Lys Asp

<400> 280

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<210> 281
<211> 471
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (1)...(471)

<400> 281

atg	aaa	ata	agc	tgc	tca	gat	ctt	ctg	ctg	cag	gga	gca	aag	ttg	atg	48
Met	Lys	Ile	Ser	Cys	Ser	Asp	Leu	Leu	Leu	Gln	Gly	Ala	Lys	Leu	Met	
1				5					10					15		
atg	gtt	cca	gct	gac	tcc	ctt	ctg	gat	tta	ctg	ctg	tta	acc	tgc	ctt	96
Met	Val	Pro	Ala	Asp	Ser	Leu	Leu	Asp	Leu	Leu	Leu	Leu	Thr	Cys	Leu	
			20					25					30			
cct	cag	gca	gga	gag	tct	cga	gta	gaa	ggc	aaa	gat	acc	cct	gcc	tcg	144
Pro	Gln	Ala	Gly	Glu	Ser	Arg	Val	Glu	Gly	Lys	Asp	Thr	Pro	Ala	Ser	
		35					40					45				

cct gaa cat aaa gcg gat gcg cac atc gtt aag atc cac gtg ata gag 192
 Pro Glu His Lys Ala Asp Ala His Ile Val Lys Ile His Val Ile Glu
 50 55 60

ata aat cct cga ttt aat cta ggc ggg agt gat gcg ttt ctt gtg agc 240
 Ile Asn Pro Arg Phe Asn Leu Gly Gly Ser Asp Ala Phe Leu Val Ser
 65 70 75 80

ccg att cgg caa gat tta cgt ggg cag gtc ctt tct ata ttc gag ctg 288
 Pro Ile Arg Gln Asp Leu Arg Gly Gln Val Leu Ser Ile Phe Glu Leu
 85 90 95

acc caa agc acc tta tca gat gaa agg att act cag cat caa cat tta 336
 Thr Gln Ser Thr Leu Ser Asp Glu Arg Ile Thr Gln His Gln His Leu
 100 105 110

cat agt aga ggt gag cta tct tgt gaa ccg gat gtg gag ccc tta ggc 384
 His Ser Arg Gly Glu Leu Ser Cys Glu Pro Asp Val Glu Pro Leu Gly
 115 120 125

ttc agc gcc cgg aaa ggt caa tgc ctc cgt agg gac cac agt cag att 432
 Phe Ser Ala Arg Lys Gly Gln Cys Leu Arg Arg Asp His Ser Gln Ile
 130 135 140

gca act cct cct tcg gta aat gcc gaa aaa aca acg tag 471
 Ala Thr Pro Pro Ser Val Asn Ala Glu Lys Thr Thr *
 145 150 155

<210> 282

<211> 156

<212> PRT

<213> Homo sapiens

<400> 282

Met Lys Ile Ser Cys Ser Asp Leu Leu Leu Gln Gly Ala Lys Leu Met
 1 5 10 15
 Met Val Pro Ala Asp Ser Leu Leu Asp Leu Leu Leu Leu Thr Cys Leu
 20 25 30
 Pro Gln Ala Gly Glu Ser Arg Val Glu Gly Lys Asp Thr Pro Ala Ser
 35 40 45
 Pro Glu His Lys Ala Asp Ala His Ile Val Lys Ile His Val Ile Glu
 50 55 60

Ile Asn Pro Arg Phe Asn Leu Gly Gly Ser Asp Ala Phe Leu Val Ser
 65 70 75 80
 Pro Ile Arg Gln Asp Leu Arg Gly Gln Val Leu Ser Ile Phe Glu Leu
 85 90 95
 Thr Gln Ser Thr Leu Ser Asp Glu Arg Ile Thr Gln His Gln His Leu
 100 105 110
 His Ser Arg Gly Glu Leu Ser Cys Glu Pro Asp Val Glu Pro Leu Gly
 115 120 125
 Phe Ser Ala Arg Lys Gly Gln Cys Leu Arg Arg Asp His Ser Gln Ile
 130 135 140
 Ala Thr Pro Pro Ser Val Asn Ala Glu Lys Thr Thr
 145 150 155

<210> 283
 <211> 702
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(702)

<400> 283

atg gaa ggc tcc att tat gct tgg ggc att ctc ttg atg ttg ggc gcg	48
Met Glu Gly Ser Ile Tyr Ala Trp Gly Ile Leu Leu Met Leu Gly Ala	
1 5 10 15	
ggt cct ccg ggg tgg tgt ggg ggt gtg ttg aaa tct gct cga cgt ccg	96
Val Pro Pro Gly Trp Cys Gly Gly Val Leu Lys Ser Ala Arg Arg Pro	
20 25 30	
gag aag gct acg gcc gtt gtg cta cat gag gag tgt atg cgt aaa cat	144
Glu Lys Ala Thr Ala Val Val Leu His Glu Glu Cys Met Arg Lys His	
35 40 45	
ctt gcg gct aaa ccg acc gct cta att tta aaa agg cat cgg caa gca	192
Leu Ala Ala Lys Pro Thr Ala Leu Ile Leu Lys Arg His Arg Gln Ala	
50 55 60	
ggc gcc cac aag tcg agt tac ccg ggt caa caa agc tca gcg cct acc	240
Gly Ala His Lys Ser Ser Tyr Pro Gly Gln Gln Ser Ser Ala Pro Thr	
65 70 75 80	

$\langle 210 \rangle$	284
$\langle 211 \rangle$	233

<400> 285

atg	ccc	tgt	gcc	ctt	tgg	gaa	cat	aag	aac	aaa	gta	cgc	ctg	tct	ccc	48
Met	Pro	Cys	Ala	Leu	Trp	Glu	His	Lys	Asn	Lys	Val	Arg	Leu	Ser	Pro	
1				5				10					15			

ctc	tca	tcg	ttg	tta	ctg	ttg	ctt	cat	cca	gga	tat	ggg	gga	cag	tca	96
Leu	Ser	Ser	Leu	Leu	Leu	Leu	Leu	His	Pro	Gly	Tyr	Gly	Gly	Gln	Ser	
			20					25					30			

gaa	tcc	gaa	agc	ttg	cag	caa	aat	ggc	tgg	ctt	tac	ctt	att	ttg	gag	144
Glu	Ser	Glu	Ser	Leu	Gln	Gln	Asn	Gly	Trp	Leu	Tyr	Leu	Ile	Leu	Glu	
		35					40					45				

gga	ata	tat	ttt	ctg	aaa	gtt	cag	gcc	tgg	gta	att	cca	aat	gac	aat	192
Gly	Ile	Tyr	Phe	Leu	Lys	Val	Gln	Ala	Trp	Val	Ile	Pro	Asn	Asp	Asn	
	50					55					60					

ctg	aat	aga	atg	tta	ttg	gca	gaa	gtg	aac	aaa	tat	gaa	aat	gtt	ctc	240
Leu	Asn	Arg	Met	Leu	Leu	Ala	Glu	Val	Asn	Lys	Tyr	Glu	Asn	Val	Leu	
65					70				75						80	

gta	att	aag	gtc	cta	gga	gag	tta	cat	ggg	aca	ccc	aag	agt	gct	tat	288
Val	Ile	Lys	Val	Leu	Gly	Glu	Leu	His	Gly	Thr	Pro	Lys	Ser	Ala	Tyr	
			85						90					95		

gag	aaa	gtt	tgg	ggc	att	gct	gat	agc	aat	cag	aat	cag	aaa	tgt	acc	336
Glu	Lys	Val	Trp	Gly	Ile	Ala	Asp	Ser	Asn	Gln	Asn	Gln	Lys	Cys	Thr	
			100					105					110			

tgc	tca	gat	tat	cca	tat	aaa	caa	ttg	aaa	taa						369
Cys	Ser	Asp	Tyr	Pro	Tyr	Lys	Gln	Leu	Lys	*						
		115					120									

<210> 286

<211> 122

<212> PRT

<213> Homo sapiens

<400> 286

Met	Pro	Cys	Ala	Leu	Trp	Glu	His	Lys	Asn	Lys	Val	Arg	Leu	Ser	Pro
1				5				10					15		

"069973" 22222222

Leu Ser Ser Leu Leu Leu Leu Leu His Pro Gly Tyr Gly Gly Gln Ser
 20 25 30
 Glu Ser Glu Ser Leu Gln Gln Asn Gly Trp Leu Tyr Leu Ile Leu Glu
 35 40 45
 Gly Ile Tyr Phe Leu Lys Val Gln Ala Trp Val Ile Pro Asn Asp Asn
 50 55 60
 Leu Asn Arg Met Leu Leu Ala Glu Val Asn Lys Tyr Glu Asn Val Leu
 65 70 75 80
 Val Ile Lys Val Leu Gly Glu Leu His Gly Thr Pro Lys Ser Ala Tyr
 85 90 95
 Glu Lys Val Trp Gly Ile Ala Asp Ser Asn Gln Asn Gln Lys Cys Thr
 100 105 110
 Cys Ser Asp Tyr Pro Tyr Lys Gln Leu Lys
 115 120

<210> 287

<211> 486

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(486)

<400> 287

atg ggg aaa ctc ttg act ttg gtc agc atg ctc cta agt gga ctg cag 48
 Met Gly Lys Leu Leu Thr Leu Val Ser Met Leu Leu Ser Gly Leu Gln
 1 5 10 15

gct atg tgg gaa ctg gtg tat aga act att ggg cac caa ctt cac tgg 96
 Ala Met Trp Glu Leu Val Tyr Arg Thr Ile Gly His Gln Leu His Trp
 20 25 30

atc agt ggc tat ata gcg acg gtt gta cga ggg ttt cgc cac gtc aca 144
 Ile Ser Gly Tyr Ile Ala Thr Val Val Arg Gly Phe Arg His Val Thr
 35 40 45

caa ggt gat tgc aaa cat tat gtg atc ctc aca aac aca ggt tgt atc 192
 Gln Gly Asp Cys Lys His Tyr Val Ile Leu Thr Asn Thr Gly Cys Ile
 50 55 60

tgt ggt gga caa gtt atg tgg act gta cct tat tgt tat cct ggt gtg 240
 Cys Gly Gly Gln Val Met Trp Thr Val Pro Tyr Cys Tyr Pro Gly Val

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<210> 288
<211> 161
<212> PRT
<213> Homo sapiens

<400> 288
Met Gly Lys Leu Leu Thr Leu Val Ser Met Leu Leu Ser Gly Leu Gln
 1          5          10          15
Ala Met Trp Glu Leu Val Tyr Arg Thr Ile Gly His Gln Leu His Trp
 20          25          30
Ile Ser Gly Tyr Ile Ala Thr Val Val Arg Gly Phe Arg His Val Thr
 35          40          45
Gln Gly Asp Cys Lys His Tyr Val Ile Leu Thr Asn Thr Gly Cys Ile
 50          55          60
Cys Gly Gly Gln Val Met Trp Thr Val Pro Tyr Cys Tyr Pro Gly Val
 65          70          75          80

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Ser Ser Val Gly Cys Ile Asn Cys Leu Pro Ile Leu Ser Pro Leu Arg
 85 90 95
 Leu Ser Asn Leu Cys Val Leu Phe Asn Ala Met Arg Gly Arg Arg Asn
 100 105 110
 Lys Val Phe Val Ser Pro Glu Asp Leu Thr Arg Leu Gly Gly Glu Lys
 115 120 125
 Gly Gly Thr Arg Arg Ala Glu Glu Gly Arg Glu Thr Glu Lys Glu His
 130 135 140
 Ile Glu Asp Arg Lys Arg Lys Arg Arg Lys Glu Ile Val Asn Lys Glu
 145 150 155 160
 Lys

<210> 289
 <211> 651
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(651)

<400> 289

atg agg ggc acc cac atc ctc atg ggg ctg agt ctc ttc tat ccc atc	48
Met Arg Gly Thr His Ile Leu Met Gly Leu Ser Leu Phe Tyr Pro Ile	
1 5 10 15	
aga gcc ctg gaa aca ggg acc caa gtg gtc tgc ggc cac cag ccc tgg	96
Arg Ala Leu Glu Thr Gly Thr Gln Val Val Cys Gly His Gln Pro Trp	
20 25 30	
tgt ggc ctg aag gct ggg cgt cta ggc ctc cgg cct cca ccc cct ctg	144
Cys Gly Leu Lys Ala Gly Arg Leu Gly Leu Arg Pro Pro Pro Pro Leu	
35 40 45	
tgc agt ggg cag tca cac ctg gcg ggg ccc ggc tgc ctg ccc aga cag	192
Cys Ser Gly Gln Ser His Leu Ala Gly Pro Gly Cys Leu Pro Arg Gln	
50 55 60	
cag gtt ctc agc agc agc cct ggc gtc cca gga gag ggg ctt ctc tct	240
Gln Val Leu Ser Ser Ser Pro Gly Val Pro Gly Glu Gly Leu Leu Ser	
65 70 75 80	

Met Arg Gly Thr His Ile Leu Met Gly Leu Ser Leu Phe Tyr Pro Ile
 1 5 10 15
 Arg Ala Leu Glu Thr Gly Thr Gln Val Val Cys Gly His Gln Pro Trp
 20 25 30
 Cys Gly Leu Lys Ala Gly Arg Leu Gly Leu Arg Pro Pro Pro Leu
 35 40 45
 Cys Ser Gly Gln Ser His Leu Ala Gly Pro Gly Cys Leu Pro Arg Gln
 50 55 60
 Gln Val Leu Ser Ser Ser Pro Gly Val Pro Gly Glu Gly Leu Leu Ser
 65 70 75 80
 Ala Pro Gly Phe Gln Glu His Arg Asp Ala Trp Val Cys Ser His Asp
 85 90 95
 Leu Gly Ser Cys Ile Cys Ala Gln Arg Gly Gly Ala Pro Ala Cys Ser
 100 105 110
 Met Glu Gln Lys Ala Trp Ile Cys Ser Trp Asp Leu Gly Gly Ala Ser
 115 120 125
 Ala Cys Ser Val Glu Gln Glu Val Trp Val Tyr Ser Cys Asp Phe Ser
 130 135 140
 Gly Cys Ser Cys Ala Gln Glu Ser Gly Ala Pro Ile Cys Ser Arg Pro
 145 150 155 160
 Glu Ser Thr Gly Met Pro Lys Ser Ala Glu Ser Tyr His Pro Pro Arg
 165 170 175
 Lys Gly Gln Gly Leu Cys Leu Ser Ala Ala Pro Ala Ser Ser Met Glu
 180 185 190
 His Ala Ala Leu Ala Val Ala Ala Cys Cys Ser Trp His Asp Gly Thr
 195 200 205
 Ser His Phe Arg Trp Thr Arg Val
 210 215

<210> 291

<211> 708

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(708)

<400> 291

atg cgg cct gat gac att aac ccg agg act ggg ctg gtg gtg gcc ctg
 Met Arg Pro Asp Asp Ile Asn Pro Arg Thr Gly Leu Val Val Ala Leu
 1 5 10 15

gtc agt gtc ttc ctc gtc ttt ggt ttc atg ttc acc gtc tct ggg atg Val Ser Val Phe Leu Val Phe Gly Phe Met Phe Thr Val Ser Gly Met 20 25 30	96
aaa ggg gag act ttg gga aac atc ccc ctc ctg gcc atc ggg cca gcc Lys Gly Glu Thr Leu Gly Asn Ile Pro Leu Leu Ala Ile Gly Pro Ala 35 40 45	144
atc tgc cta cca ggc atc gca gcc att gcc ctg gcc agg aaa acc gag Ile Cys Leu Pro Gly Ile Ala Ala Ile Ala Leu Ala Arg Lys Thr Glu 50 55 60	192
gga tgc acc aag tgg cca gag aac gag ctg ctg tgg gtc cgc aaa ttg Gly Cys Thr Lys Trp Pro Glu Asn Glu Leu Leu Trp Val Arg Lys Leu 65 70 75 80	240
ccc tgc ttc cgg aaa ccc aaa gac aag gag gtg gta gag ctg ctg agg Pro Cys Phe Arg Lys Pro Lys Asp Lys Glu Val Val Glu Leu Leu Arg 85 90 95	288
acc cct tca gac cta gaa tcc ggc aag ggg agc tca gat gag ctg gct Thr Pro Ser Asp Leu Glu Ser Gly Lys Gly Ser Ser Asp Glu Leu Ala 100 105 110	336
aag aag gcg ggc ctc agg ggg aag cct ccc cca caa agc cag ggt gag Lys Lys Ala Gly Leu Arg Gly Lys Pro Pro Pro Gln Ser Gln Gly Glu 115 120 125	384
gtg tcc gtg gcc agc tcc atc aac agc ccc aca ccc acg gag gaa gga Val Ser Val Ala Ser Ser Ile Asn Ser Pro Thr Pro Thr Glu Glu Gly 130 135 140	432
gaa tgc cag agc ctc gtc cag aat ggg cat cag gag gag acg tcc aga Glu Cys Gln Ser Leu Val Gln Asn Gly His Gln Glu Glu Thr Ser Arg 145 150 155 160	480
tac ctg gac ggc tac tgc ccc tcg ggc agt tcc ctc acc tac agt gcc Tyr Leu Asp Gly Tyr Cys Pro Ser Gly Ser Ser Leu Thr Tyr Ser Ala 165 170 175	528
ttg gac gtc aag tgc tca gca agg gac aga tct gag tgc cct gag cct Leu Asp Val Lys Cys Ser Ala Arg Asp Arg Ser Glu Cys Pro Glu Pro 180 185 190	576

gag gat agc atc ttc ttt gtg ccc cag gac agt atc atc gtt tgc tcc 624
 Glu Asp Ser Ile Phe Phe Val Pro Gln Asp Ser Ile Ile Val Cys Ser
 195 200 205

 tac aag cag aac agc ccg tat gac aga tac tgt tgt tat atc aat cag 672
 Tyr Lys Gln Asn Ser Pro Tyr Asp Arg Tyr Cys Cys Tyr Ile Asn Gln
 210 215 220

 ata caa ggc agg tgg gac cac gag acc atc gtc taa 708
 Ile Gln Gly Arg Trp Asp His Glu Thr Ile Val *
 225 230 235

<210> 292
 <211> 235
 <212> PRT
 <213> Homo sapiens

<400> 292
 Met Arg Pro Asp Asp Ile Asn Pro Arg Thr Gly Leu Val Val Ala Leu
 1 5 10 15
 Val Ser Val Phe Leu Val Phe Gly Phe Met Phe Thr Val Ser Gly Met
 20 25 30
 Lys Gly Glu Thr Leu Gly Asn Ile Pro Leu Leu Ala Ile Gly Pro Ala
 35 40 45
 Ile Cys Leu Pro Gly Ile Ala Ala Ile Ala Leu Ala Arg Lys Thr Glu
 50 55 60
 Gly Cys Thr Lys Trp Pro Glu Asn Glu Leu Leu Trp Val Arg Lys Leu
 65 70 75 80
 Pro Cys Phe Arg Lys Pro Lys Asp Lys Glu Val Val Glu Leu Leu Arg
 85 90 95
 Thr Pro Ser Asp Leu Glu Ser Gly Lys Gly Ser Ser Asp Glu Leu Ala
 100 105 110
 Lys Lys Ala Gly Leu Arg Gly Lys Pro Pro Pro Gln Ser Gln Gly Glu
 115 120 125
 Val Ser Val Ala Ser Ser Ile Asn Ser Pro Thr Pro Thr Glu Glu Gly
 130 135 140
 Glu Cys Gln Ser Leu Val Gln Asn Gly His Gln Glu Glu Thr Ser Arg
 145 150 155 160
 Tyr Leu Asp Gly Tyr Cys Pro Ser Gly Ser Ser Leu Thr Tyr Ser Ala
 165 170 175
 Leu Asp Val Lys Cys Ser Ala Arg Asp Arg Ser Glu Cys Pro Glu Pro

Ile	Ile	Phe	Leu	Ala	Glu	Leu	Ser	Ala	Ala	Ile	Leu	Ala	Phe	Ile	Phe		
			100					105					110				
agg	gaa	aat	gta	cgt	atc	agg	ccc	caa	gct	ttc	ctg	cct	cct	gct	atc	384	
Arg	Glu	Asn	Val	Arg	Ile	Arg	Pro	Gln	Ala	Phe	Leu	Pro	Pro	Ala	Ile		
		115					120					125					
agc	aag	ggg	ttg	gtg	gcc	att	cag	ctc	acc	cga	gaa	ttc	ttc	acc	aag	432	
Ser	Lys	Gly	Leu	Val	Ala	Ile	Gln	Leu	Thr	Arg	Glu	Phe	Phe	Thr	Lys		
	130					135					140						
gag	ctc	acc	aag	cac	tac	cag	ggc	aat	aac	gac	aca	gac	gtc	ttc	tct	480	
Glu	Leu	Thr	Lys	His	Tyr	Gln	Gly	Asn	Asn	Asp	Thr	Asp	Val	Phe	Ser		
145					150					155					160		
gcc	acc	tgg	aac	tcg	gtc	atg	atc	aca	ttt	ggt	tgc	tgc	ggg	gtc	aac	528	
Ala	Thr	Trp	Asn	Ser	Val	Met	Ile	Thr	Phe	Gly	Cys	Cys	Gly	Val	Asn		
				165					170					175			
ggg	cct	gaa	gac	ttt	aag	ttt	gca	tct	gtg	ttt	cga	ctc	ctg	acc	ctg	576	
Gly	Pro	Glu	Asp	Phe	Lys	Phe	Ala	Ser	Val	Phe	Arg	Leu	Leu	Thr	Leu		
			180					185						190			
gat	agt	gaa	gag	gtg	ccg	gag	gcc	tgc	tgc	cgg	agg	gaa	ccc	caa	agt	624	
Asp	Ser	Glu	Glu	Val	Pro	Glu	Ala	Cys	Cys	Arg	Arg	Glu	Pro	Gln	Ser		
		195					200					205					
cgg	gac	ggg	gtc	ctg	ctg	agc	cgg	gag	gag	tgc	ctc	ctg	gga	agg	agc	672	
Arg	Asp	Gly	Val	Leu	Leu	Ser	Arg	Glu	Glu	Cys	Leu	Leu	Gly	Arg	Ser		
	210					215					220						
cta	ttc	cta	aac	aag	cag	ggc	tgt	tac	acg	gtg	atc	ctc	aac	acc	ttc	720	
Leu	Phe	Leu	Asn	Lys	Gln	Gly	Cys	Tyr	Thr	Val	Ile	Leu	Asn	Thr	Phe		
225					230					235					240		
gag	acc	tac	gtc	tac	ttg	gcc	gga	gcc	ctt	gcc	atc	ggg	gta	ctg	gcc	768	
Glu	Thr	Tyr	Val	Tyr	Leu	Ala	Gly	Ala	Leu	Ala	Ile	Gly	Val	Leu	Ala		
				245				250						255			
atc	gag	ctt	ttc	gcc	atg	atc	ttt	gcc	atg	tgc	ctc	ttc	cgg	ggc	atc	816	
Ile	Glu	Leu	Phe	Ala	Met	Ile	Phe	Ala	Met	Cys	Leu	Phe	Arg	Gly	Ile		
			260					265					270				

cag tag
Gln *

822

<210> 294
<211> 273
<212> PRT
<213> Homo sapiens

<400> 294

Met	Val	Asp	Pro	Thr	Gly	Phe	Arg	Glu	Ile	Val	Ala	Ala	Asn	Pro	Leu
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Leu	Leu	Thr	Gly	Ala	Tyr	Ile	Leu	Leu	Ala	Met	Gly	Gly	Leu	Leu	Phe
			20					25					30		
Leu	Leu	Gly	Phe	Leu	Gly	Cys	Cys	Gly	Ala	Val	Arg	Glu	Asn	Lys	Cys
		35				40						45			
Leu	Leu	Leu	Phe	Leu	Pro	Gln	Leu	Arg	Lys	Gly	Glu	Thr	Thr	Gln	Lys
		50				55					60				
Arg	Asp	Arg	Glu	Asn	Ser	Val	Arg	Cys	Pro	Ala	Val	Pro	Cys	Glu	Ser
65					70					75				80	
Arg	Ser	Leu	Cys	Arg	Ser	Arg	Trp	Ser	Pro	Phe	Phe	Leu	Phe	Ile	Leu
			85					90						95	
Ile	Ile	Phe	Leu	Ala	Glu	Leu	Ser	Ala	Ala	Ile	Leu	Ala	Phe	Ile	Phe
			100					105					110		
Arg	Glu	Asn	Val	Arg	Ile	Arg	Pro	Gln	Ala	Phe	Leu	Pro	Pro	Ala	Ile
		115					120					125			
Ser	Lys	Gly	Leu	Val	Ala	Ile	Gln	Leu	Thr	Arg	Glu	Phe	Phe	Thr	Lys
	130					135					140				
Glu	Leu	Thr	Lys	His	Tyr	Gln	Gly	Asn	Asn	Asp	Thr	Asp	Val	Phe	Ser
145					150					155				160	
Ala	Thr	Trp	Asn	Ser	Val	Met	Ile	Thr	Phe	Gly	Cys	Cys	Gly	Val	Asn
			165					170					175		
Gly	Pro	Glu	Asp	Phe	Lys	Phe	Ala	Ser	Val	Phe	Arg	Leu	Leu	Thr	Leu
		180						185				190			
Asp	Ser	Glu	Glu	Val	Pro	Glu	Ala	Cys	Cys	Arg	Arg	Glu	Pro	Gln	Ser
	195						200					205			
Arg	Asp	Gly	Val	Leu	Leu	Ser	Arg	Glu	Glu	Cys	Leu	Leu	Gly	Arg	Ser
	210					215					220				
Leu	Phe	Leu	Asn	Lys	Gln	Gly	Cys	Tyr	Thr	Val	Ile	Leu	Asn	Thr	Phe
225					230					235				240	
Glu	Thr	Tyr	Val	Tyr	Leu	Ala	Gly	Ala	Leu	Ala	Ile	Gly	Val	Leu	Ala
			245					250						255	

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F09990.226550

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<210> 295
<211> 567
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(567)

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<400> 295																
atg	agc	aga	gac	cac	agg	ctg	ctg	tgc	ctc	ctg	ggc	ctc	tgt	tgt	gtg	48
Met	Ser	Arg	Asp	His	Arg	Leu	Leu	Cys	Leu	Leu	Gly	Leu	Cys	Cys	Val	
1			5			10			15							
>400 300																
gca	gat	gct	tcc	aaa	cag	ccc	ttc	agg	aaa	tct	gga	att	ccc	aga	ggt	96
Ala	Asp	Ala	Ser	Lys	Gln	Pro	Phe	Arg	Lys	Ser	Gly	Ile	Pro	Arg	Gly	
			20			25			30							
>400 305																
tat	aca	ttg	cac	ctg	agg	cca	tct	ggc	tac	aat	cca	aac	tct	ggg	tgc	144
Tyr	Thr	Leu	His	Leu	Arg	Pro	Ser	Gly	Tyr	Asn	Pro	Asn	Ser	Gly	Cys	
35			40			45										
>400 310																
ggc	tgg	cgc	caa	agc	tac	tac	acc	atg	ctg	cct	tct	aag	ctg	cat	ttc	192
Gly	Trp	Arg	Gln	Ser	Tyr	Tyr	Thr	Met	Leu	Pro	Ser	Lys	Leu	His	Phe	
50			55			60										
>400 315																
atc	tgg	aac	cgc	tgt	ggc	tgg	cag	gcc	gag	cct	ctg	aac	act	gca	att	240
Ile	Trp	Asn	Arg	Cys	Gly	Trp	Gln	Ala	Glu	Pro	Leu	Asn	Thr	Ala	Ile	
65			70			75			80							
>400 320																
cag	gtt	aat	cat	gca	gac	ctg	ctg	gag	cac	gcg	ggg	ccg	agg	gga	ggc	288
Gln	Val	Asn	His	Ala	Asp	Leu	Leu	Glu	His	Ala	Gly	Pro	Arg	Gly	Gly	
			85			90			95							
>400 325																
cca	cac	tac	cgc	ttt	ccc	cac	tct	ggg	gac	ggg	gag	aac	ctg	att	tgt	336
Pro	His	Tyr	Arg	Phe	Pro	His	Ser	Gly	Asp	Gly	Glu	Asn	Leu	Ile	Cys	
			100			105			110							

ctt cgg tcc aca gct agt gtg tgc aag ggc cca att cag gtc cag atc 384
 Leu Arg Ser Thr Ala Ser Val Cys Lys Gly Pro Ile Gln Val Gln Ile
 115 120 125

ggc gtg ctg aca agg act gtg ttt ggg gct gct ccc ctg cag aca gag 432
 Gly Val Leu Thr Arg Thr Val Phe Gly Ala Ala Pro Leu Gln Thr Glu
 130 135 140

ccc cat ggg cag gcc ctg atg ggc ggt cag agg aca caa gac aag agc 480
 Pro His Gly Gln Ala Leu Met Gly Gly Gln Arg Thr Gln Asp Lys Ser
 145 150 155 160

cag ggt gct aag cag acg ccc cta tgg gac atg ggc cag ccg atg ttt 528
 Gln Gly Ala Lys Gln Thr Pro Leu Trp Asp Met Gly Gln Pro Met Phe
 165 170 175

gga tgc ttc caa aca cca aca aca gtt ttg gac gag taa 567
 Gly Cys Phe Gln Thr Pro Thr Thr Val Leu Asp Glu *
 180 185

<210> 296

<211> 188

<212> PRT

<213> Homo sapiens

<400> 296

Met Ser Arg Asp His Arg Leu Leu Cys Leu Leu Gly Leu Cys Cys Val
 1 5 10 15
 Ala Asp Ala Ser Lys Gln Pro Phe Arg Lys Ser Gly Ile Pro Arg Gly
 20 25 30
 Tyr Thr Leu His Leu Arg Pro Ser Gly Tyr Asn Pro Asn Ser Gly Cys
 35 40 45
 Gly Trp Arg Gln Ser Tyr Tyr Thr Met Leu Pro Ser Lys Leu His Phe
 50 55 60
 Ile Trp Asn Arg Cys Gly Trp Gln Ala Glu Pro Leu Asn Thr Ala Ile
 65 70 75 80
 Gln Val Asn His Ala Asp Leu Leu Glu His Ala Gly Pro Arg Gly Gly
 85 90 95
 Pro His Tyr Arg Phe Pro His Ser Gly Asp Gly Glu Asn Leu Ile Cys
 100 105 110
 Leu Arg Ser Thr Ala Ser Val Cys Lys Gly Pro Ile Gln Val Gln Ile
 115 120 125

ctg att gct gtg gtg ggc tcc ctg gcc ttt ctg ctg atg ttc atc gtc 336
 Leu Ile Ala Val Val Gly Ser Leu Ala Phe Leu Leu Met Phe Ile Val
 100 105 110

tgt gcc gcg gtc atc acc cgg cag aag cag aag gcc tcg gcc tat tac 384
 Cys Ala Ala Val Ile Thr Arg Gln Lys Gln Lys Ala Ser Ala Tyr Tyr
 115 120 125

cca tcg tcc ttc ccc aag aag aag tac gtg gac cag agt gac cgg gcc 432
 Pro Ser Ser Phe Pro Lys Lys Lys Tyr Val Asp Gln Ser Asp Arg Ala
 130 135 140

ggg ggc ccc cgg gcc ttc agt gag gtc ccc gac aga gcc ccc gac agc 480
 Gly Gly Pro Arg Ala Phe Ser Glu Val Pro Asp Arg Ala Pro Asp Ser
 145 150 155 160

agg ccc gag gaa gcc ctg gat tcc tcc cgg cag ctc cag gcc gac atc 528
 Arg Pro Glu Glu Ala Leu Asp Ser Ser Arg Gln Leu Gln Ala Asp Ile
 165 170 175

ttg gcc gcc acc cag aac ctc aag tcc ccc acc agg gct gca ctg ggc 576
 Leu Ala Ala Thr Gln Asn Leu Lys Ser Pro Thr Arg Ala Ala Leu Gly
 180 185 190

ggt ggg gac gga gcc agg atg gtg gag ggc agg ggc gca gag gaa gag 624
 Gly Gly Asp Gly Ala Arg Met Val Glu Gly Arg Gly Ala Glu Glu Glu
 195 200 205

gag aag ggc agc cag gag ggg gac cag gaa gtc cag gga cat ggg gtc 672
 Glu Lys Gly Ser Gln Glu Gly Asp Gln Glu Val Gln Gly His Gly Val
 210 215 220

cca gtg gag aca cca gag gcg cag gag gag ccg tgc tca ggg gtc ctt 720
 Pro Val Glu Thr Pro Glu Ala Gln Glu Glu Pro Cys Ser Gly Val Leu
 225 230 235 240

gag ggg gct gtg gtg gcc ggt gag ggc caa ggg gag ctg gaa ggg tct 768
 Glu Gly Ala Val Val Ala Gly Glu Gly Gln Gly Glu Leu Glu Gly Ser
 245 250 255

ctc ttg tta gcc cag gaa gcc cag gga cca gtg ggt ccc ccc gaa agc 816
 Leu Leu Leu Ala Gln Glu Ala Gln Gly Pro Val Gly Pro Pro Glu Ser
 260 265 270


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<210> 299
<211> 369
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> (1)...(369)
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<400> 299																
atg	gcc	ctg	ggc	aag	gtt	ctg	gcc	atg	gca	ctg	gtt	ttg	gcc	ttg	gcc	48
Met	Ala	Leu	Gly	Lys	Val	Leu	Ala	Met	Ala	Leu	Val	Leu	Ala	Leu	Ala	
1			5			10			15							
<400> 96																
gtg	ctg	ggg	tcg	ctg	tcc	cct	ggg	gcc	cgg	gcg	ggg	gac	tgc	aag	ggg	96
Val	Leu	Gly	Ser	Leu	Ser	Pro	Gly	Ala	Arg	Ala	Gly	Asp	Cys	Lys	Gly	
			20			25			30							
<400> 144																
cag	cgg	cag	gtg	ctg	cgg	gag	gcg	cca	ggc	ttc	gtg	acg	gat	ggg	gcg	144
Gln	Arg	Gln	Val	Leu	Arg	Glu	Ala	Pro	Gly	Phe	Val	Thr	Asp	Gly	Ala	
35						40						45				
<400> 192																
ggc	aac	tac	agc	gtc	aat	ggc	aac	tgc	gag	tgg	ctc	atc	gag	gaa	ccc	192
Gly	Asn	Tyr	Ser	Val	Asn	Gly	Asn	Cys	Glu	Trp	Leu	Ile	Glu	Glu	Pro	
50						55			60							
<400> 240																
tgc	ccc	agt	ggc	tct	ttc	tct	gtg	aag	aca	tgt	ggc	tta	acc	tgg	ggg	240
Cys	Pro	Ser	Gly	Ser	Phe	Ser	Val	Lys	Thr	Cys	Gly	Leu	Thr	Trp	Gly	
65			70			75			80							
<400> 288																
ata	gct	gag	atc	aga	ggc	atc	tgt	acg	agg	gag	cag	aag	ggc	att	cca	288
Ile	Ala	Glu	Ile	Arg	Gly	Ile	Cys	Thr	Arg	Glu	Gln	Lys	Gly	Ile	Pro	
			85			90						95				
<400> 336																
ggc	aag	aat	agc	tgt	gca	aag	gcg	ggg	aag	cgg	gag	agt	gat	gct	ttt	336
Gly	Lys	Asn	Ser	Cys	Ala	Lys	Ala	Gly	Lys	Arg	Glu	Ser	Asp	Ala	Phe	
			100			105			110							

369

```
<210> 300
<211> 122
<212> PRT
<213> Homo sapiens
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<400> 300															
Met	Ala	Leu	Gly	Lys	Val	Leu	Ala	Met	Ala	Leu	Val	Leu	Ala	Leu	Ala
1				5				10						15	
Val	Leu	Gly	Ser	Leu	Ser	Pro	Gly	Ala	Arg	Ala	Gly	Asp	Cys	Lys	Gly
			20					25					30		
Gln	Arg	Gln	Val	Leu	Arg	Glu	Ala	Pro	Gly	Phe	Val	Thr	Asp	Gly	Ala
		35					40					45			
Gly	Asn	Tyr	Ser	Val	Asn	Gly	Asn	Cys	Glu	Trp	Leu	Ile	Glu	Glu	Pro
	50					55					60				
Cys	Pro	Ser	Gly	Ser	Phe	Ser	Val	Lys	Thr	Cys	Gly	Leu	Thr	Trp	Gly
65					70					75					80
Ile	Ala	Glu	Ile	Arg	Gly	Ile	Cys	Thr	Arg	Glu	Gln	Lys	Gly	Ile	Pro
			85					90						95	
Gly	Lys	Asn	Ser	Cys	Ala	Lys	Ala	Gly	Lys	Arg	Glu	Ser	Asp	Ala	Phe
			100					105					110		
Glu	Glu	Leu	Glu	Ile	Gln	Cys	Val	Lys	Thr						
		115					120								

```
<210> 301
<211> 411
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (1)...(411)

<400> 301
atg gac gca tac agc gcg tct tta agc ggt ccc aac agc ctc ggg ctg . 48
Met Asp Ala Tyr Ser Ala Ser Leu Ser Gly Pro Asn Ser Leu Gly Leu
1 5 10 15

tcc act tta gta ccc cca agc aat gcg cga gag tgc ccg acg gaa cca 96
 Ser Thr Leu Val Pro Pro Ser Asn Ala Arg Glu Cys Pro Thr Glu Pro
 20 25 30

cca aag ata ctg tct ctg tca gtt cca cca agc cct gca gta gaa cct 144
 Pro Lys Ile Leu Ser Leu Ser Val Pro Pro Ser Pro Ala Val Glu Pro
 35 40 45

aga ccc aga tgg aaa gag aac aag aca aaa tca gga agt aga ggc agc 192
 Arg Pro Arg Trp Lys Glu Asn Lys Thr Lys Ser Gly Ser Arg Gly Ser
 50 55 60

tct agt gct gac aac tgc cag gga agc aat gag ctg aat ggg ttc cct 240
 Ser Ser Ala Asp Asn Cys Gln Gly Ser Asn Glu Leu Asn Gly Phe Pro
 65 70 75 80

gaa gcc gcc ata aca aag acc aca aag tta gtt tca caa caa atg tat 288
 Glu Ala Ala Ile Thr Lys Thr Thr Lys Leu Val Ser Gln Gln Met Tyr
 85 90 95

att gag tgc ctg ctc cac acc agg cac tgt tgt agg ccc cgg gag tac 336
 Ile Glu Cys Leu Leu His Thr Arg His Cys Cys Arg Pro Arg Glu Tyr
 100 105 110

agc tgt gaa caa aac agt gaa gat act tca tca gag aca gtt tgc gga 384
 Ser Cys Glu Gln Asn Ser Glu Asp Thr Ser Ser Glu Thr Val Cys Gly
 115 120 125

gat gaa aat gct cct caa gag ctt tga 411
 Asp Glu Asn Ala Pro Gln Glu Leu *
 130 135

<210> 302

<211> 136

<212> PRT

<213> Homo sapiens

<400> 302

Met Asp Ala Tyr Ser Ala Ser Leu Ser Gly Pro Asn Ser Leu Gly Leu
 1 5 10 15
 Ser Thr Leu Val Pro Pro Ser Asn Ala Arg Glu Cys Pro Thr Glu Pro
 20 25 30

Pro Lys Ile Leu Ser Leu Ser Val Pro Pro Ser Pro Ala Val Glu Pro
 35 40 45
 Arg Pro Arg Trp Lys Glu Asn Lys Thr Lys Ser Gly Ser Arg Gly Ser
 50 55 60
 Ser Ser Ala Asp Asn Cys Gln Gly Ser Asn Glu Leu Asn Gly Phe Pro
 65 70 75 80
 Glu Ala Ala Ile Thr Lys Thr Thr Lys Leu Val Ser Gln Gln Met Tyr
 85 90 95
 Ile Glu Cys Leu Leu His Thr Arg His Cys Cys Arg Pro Arg Glu Tyr
 100 105 110
 Ser Cys Glu Gln Asn Ser Glu Asp Thr Ser Ser Glu Thr Val Cys Gly
 115 120 125
 Asp Glu Asn Ala Pro Gln Glu Leu
 130 135

<210> 303

<211> 915

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(915)

<400> 303

atg ctg ccg ccg ccg cgg ccc gca gct gcc ttg gcg ctg cct gtg ctc 48
 Met Leu Pro Pro Pro Arg Pro Ala Ala Ala Leu Ala Leu Pro Val Leu
 1 5 10 15

ctg cta ctg ctg gtg gtg ctg acg ccg ccc ccg acc ggc gca agg cca 96
 Leu Leu Leu Leu Val Val Leu Thr Pro Pro Pro Thr Gly Ala Arg Pro
 20 25 30

tcc cca ggc cca gat tac ctg cgg cgc ggc tgg atg cgg ctg cta gcg 144
 Ser Pro Gly Pro Asp Tyr Leu Arg Arg Gly Trp Met Arg Leu Leu Ala
 35 40 45

gag ggc gag ggc tgc gct ccc tgc cgg cca gaa gag tgc gcc gcg ccg 192
 Glu Gly Glu Gly Cys Ala Pro Cys Arg Pro Glu Glu Cys Ala Ala Pro
 50 55 60

cgg ggc tgc ctg gcg ggc agg gtg cgc gac gcg tgc ggc tgc tgc tgg 240
 Arg Gly Cys Leu Ala Gly Arg Val Arg Asp Ala Cys Gly Cys Cys Trp

65	70	75	80	
gaa tgc gcc aac ctc gag ggc cag ctc tgc gac ctg gac ccc agt gct				288
Glu Cys Ala Asn Leu Glu Gly Gln Leu Cys Asp Leu Asp Pro Ser Ala				
	85	90	95	
cac ttc tac ggg cac tgc ggc gag cag ctt gag tgc cgg ctg gac aca				336
His Phe Tyr Gly His Cys Gly Glu Gln Leu Glu Cys Arg Leu Asp Thr				
	100	105	110	
ggc ggc gac ctg agc cgc gga gag gtg ccg gaa cct ctg tgt gcc tgt				384
Gly Gly Asp Leu Ser Arg Gly Glu Val Pro Glu Pro Leu Cys Ala Cys				
	115	120	125	
cgt tcg cag agt ccg ctc tgc ggg tcc gac ggt cac acc tac tcc cag				432
Arg Ser Gln Ser Pro Leu Cys Gly Ser Asp Gly His Thr Tyr Ser Gln				
	130	135	140	
atc tgc cgc ctg cag gag gcg gcc cgc gct cgg ccc gat gcc aac ctc				480
Ile Cys Arg Leu Gln Glu Ala Ala Arg Ala Arg Pro Asp Ala Asn Leu				
	145	150	155	160
act gtg gca cac ccg ggg ccc tgc gaa tcg ggg ccc cag atc gtg tca				528
Thr Val Ala His Pro Gly Pro Cys Glu Ser Gly Pro Gln Ile Val Ser				
	165	170	175	
cat cca tat gac act tgg aat gtg aca ggg cag gat gtg atc ttt ggc				576
His Pro Tyr Asp Thr Trp Asn Val Thr Gly Gln Asp Val Ile Phe Gly				
	180	185	190	
tgt gaa gtg ttt gcc tac ccc atg gcc tcc atc gag tgg agg aag gat				624
Cys Glu Val Phe Ala Tyr Pro Met Ala Ser Ile Glu Trp Arg Lys Asp				
	195	200	205	
ggc ttg gac atc cag ctg cca ggg gat gac ccc cac atc tct gtg cag				672
Gly Leu Asp Ile Gln Leu Pro Gly Asp Asp Pro His Ile Ser Val Gln				
	210	215	220	
ttt agg ggt gga ccc cag agg ttt gag gtg act ggc tgg ctg cag atc				720
Phe Arg Gly Gly Pro Gln Arg Phe Glu Val Thr Gly Trp Leu Gln Ile				
	225	230	235	240
cag gct gtg cgt ccc agt gat gag ggc act tac cgc tgc ctt ggc cgc				768


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      130              135              140
Ile Cys Arg Leu Gln Glu Ala Ala Arg Ala Arg Pro Asp Ala Asn Leu
145              150              155              160
Thr Val Ala His Pro Gly Pro Cys Glu Ser Gly Pro Gln Ile Val Ser
      165              170              175
His Pro Tyr Asp Thr Trp Asn Val Thr Gly Gln Asp Val Ile Phe Gly
      180              185              190
Cys Glu Val Phe Ala Tyr Pro Met Ala Ser Ile Glu Trp Arg Lys Asp
      195              200              205
Gly Leu Asp Ile Gln Leu Pro Gly Asp Asp Pro His Ile Ser Val Gln
      210              215              220
Phe Arg Gly Gly Pro Gln Arg Phe Glu Val Thr Gly Trp Leu Gln Ile
225              230              235              240
Gln Ala Val Arg Pro Ser Asp Glu Gly Thr Tyr Arg Cys Leu Gly Arg
      245              250              255
Asn Ala Leu Gly Gln Val Glu Ala Pro Ala Ser Leu Thr Val Leu Thr
      260              265              270
Pro Asp Gln Leu Asn Ser Thr Gly Ile Pro Gln Leu Arg Ser Leu Asn
      275              280              285
Leu Val Pro Glu Glu Glu Ala Glu Ser Glu Glu Asn Asp Asp Tyr Tyr
      290              295              300

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<210> 305
<211> 645
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (1)...(645)

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<400> 305
atg ctg aat gtc tcc ggc ctc ttt gtt ctc ctc tgt ggg ctg ctt gtc      48
Met Leu Asn Val Ser Gly Leu Phe Val Leu Leu Cys Gly Leu Leu Val
  1              5              10              15

tca tcc tct gca cag gag gtc ctg gct gga gtt tct tcc cag ctc ctt      96
Ser Ser Ser Ala Gln Glu Val Leu Ala Gly Val Ser Ser Gln Leu Leu
      20              25              30

aat gat ttg act caa gga ctc ctc agg gca gac ttt ctt ccc agc ctg      144
Asn Asp Leu Thr Gln Gly Leu Leu Arg Ala Asp Phe Leu Pro Ser Leu
      35              40              45

```

gac gcc gac tcc ccc gtt tga 645
Asp Ala Asp Ser Pro Val *

210

<210> 306
 <211> 214
 <212> PRT
 <213> Homo sapiens

<400> 306

```

Met Leu Asn Val Ser Gly Leu Phe Val Leu Leu Cys Gly Leu Leu Val
 1          5          10          15
Ser Ser Ser Ala Gln Glu Val Leu Ala Gly Val Ser Ser Gln Leu Leu
 20          25          30
Asn Asp Leu Thr Gln Gly Leu Leu Arg Ala Asp Phe Leu Pro Ser Leu
 35          40          45
Gln Thr Thr Gly Leu Gln Lys Pro Leu Ser Ser Ala Phe Asp Gly Val
 50          55          60
Ser Gly Leu Leu Asp Ile Phe Gly Pro Pro Leu Thr Asn Glu Ile Asn
 65          70          75          80
Thr Val Ser Ile Gln Val Lys Asn Pro Gln Leu Leu His Val Ser Ile
 85          90          95
Glu Ser Thr Pro Gln Arg Lys Glu Ala Thr Val Gln Val Pro Phe Thr
100          105          110
Ser Glu Leu Ile Val Gln Leu Leu Thr Met Lys Pro Phe Thr Ala Asn
115          120          125
Met Gln Ser Asp Ile Lys Val Gln Ile Arg Leu Glu Lys Asn Val Gly
130          135          140
Gly Arg Tyr Glu Leu Ala Phe Gly Asn Cys Arg Leu Leu Pro Glu Ala
145          150          155          160
Ile Trp Ile Gln Thr Gly Val His Glu Lys Thr Gln Gly Ala Ile Ser
165          170          175
Ile Arg Arg Ala Ile Pro Arg Ile Val Gln Pro Thr Val Ser His Gln
180          185          190
Gln Arg Leu Gly Gly Arg Ala Arg Gln His Ser Ala Gln Arg Lys Phe
195          200          205
Asp Ala Asp Ser Pro Val
210

```

<210> 307
 <211> 480
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> (1)...(480)

<400> 307

atg	agc	caa	gtg	tta	gcg	agc	ctt	gct	ctg	agc	agt	cgt	acg	gca	cag	48
Met	Ser	Gln	Val	Leu	Ala	Ser	Leu	Ala	Leu	Ser	Ser	Arg	Thr	Ala	Gln	
1				5				10						15		

gcg	cga	aca	ttg	aac	ctg	acg	aag	agc	aga	ttt	aaa	gga	ctc	gcc	gtc	96
Ala	Arg	Thr	Leu	Asn	Leu	Thr	Lys	Ser	Arg	Phe	Lys	Gly	Leu	Ala	Val	
			20				25					30				

cct	tgg	atg	gag	aaa	acc	act	gtt	gca	cag	gta	aga	acg	gca	tat	agc	144
Pro	Trp	Met	Glu	Lys	Thr	Thr	Val	Ala	Gln	Val	Arg	Thr	Ala	Tyr	Ser	
		35					40					45				

tgg	cac	gtg	cac	tac	cac	agc	ctc	tgc	ctc	gag	tgg	cca	tgg	cag	aca	192
Trp	His	Val	His	Tyr	His	Ser	Leu	Cys	Leu	Glu	Trp	Pro	Trp	Gln	Thr	
	50					55				60						

ctg	cca	ttc	aat	cct	ggt	ctg	aac	aca	acc	ccc	ttc	cca	aca	cag	ctg	240
Leu	Pro	Phe	Asn	Pro	Gly	Leu	Asn	Thr	Thr	Pro	Phe	Pro	Thr	Gln	Leu	
65					70					75				80		

tct	aca	tcc	tac	ccg	tca	gag	cag	gca	cac	cat	gtg	aaa	ctt	ctc	tgc	288
Ser	Thr	Ser	Tyr	Pro	Ser	Glu	Gln	Ala	His	His	Val	Lys	Leu	Leu	Cys	
				85				90					95			

cat	tcc	ttg	cct	agt	ggc	tct	gta	cac	agt	gtt	cct	aag	ctc	ctc	tat	336
His	Ser	Leu	Pro	Ser	Gly	Ser	Val	His	Ser	Val	Pro	Lys	Leu	Leu	Tyr	
			100				105						110			

tgg	gct	ccc	acg	gga	ctc	tat	att	cga	gac	cac	att	cca	cct	gcc	cta	384
Trp	Ala	Pro	Thr	Gly	Leu	Tyr	Ile	Arg	Asp	His	Ile	Pro	Pro	Ala	Leu	
		115				120						125				

atc	acc	ccg	ggg	cct	agt	acc	cgg	caa	cta	gga	aca	gcc	cca	gca	ccc	432
Ile	Thr	Pro	Gly	Pro	Ser	Thr	Arg	Gln	Leu	Gly	Thr	Ala	Pro	Ala	Pro	
	130					135				140						

ctg	aac	cca	cta	caa	tta	ttc	aaa	cta	gcc	agt	gct	aaa	cct	gct	taa	480
Leu	Asn	Pro	Leu	Gln	Leu	Phe	Lys	Leu	Ala	Ser	Ala	Lys	Pro	Ala	*	

145

150

155

<210> 308

<211> 159

<212> PRT

<213> Homo sapiens

<400> 308

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Met Ser Gln Val Leu Ala Ser Leu Ala Leu Ser Ser Arg Thr Ala Gln
 1          5          10          15
Ala Arg Thr Leu Asn Leu Thr Lys Ser Arg Phe Lys Gly Leu Ala Val
          20          25          30
Pro Trp Met Glu Lys Thr Thr Val Ala Gln Val Arg Thr Ala Tyr Ser
          35          40          45
Trp His Val His Tyr His Ser Leu Cys Leu Glu Trp Pro Trp Gln Thr
          50          55          60
Leu Pro Phe Asn Pro Gly Leu Asn Thr Thr Pro Phe Pro Thr Gln Leu
65          70          75          80
Ser Thr Ser Tyr Pro Ser Glu Gln Ala His His Val Lys Leu Leu Cys
          85          90          95
His Ser Leu Pro Ser Gly Ser Val His Ser Val Pro Lys Leu Leu Tyr
          100          105          110
Trp Ala Pro Thr Gly Leu Tyr Ile Arg Asp His Ile Pro Pro Ala Leu
          115          120          125
Ile Thr Pro Gly Pro Ser Thr Arg Gln Leu Gly Thr Ala Pro Ala Pro
          130          135          140
Leu Asn Pro Leu Gln Leu Phe Lys Leu Ala Ser Ala Lys Pro Ala
145          150          155

```

<210> 309

<211> 907

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(907)

<400> 309

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atg ctg ttc ctc gtc ctc ctg ctg ccc ctg gag ctg agc ctg gca ggc
Met Leu Phe Leu Val Leu Leu Leu Pro Leu Glu Leu Ser Leu Ala Gly
 1          5          10          15

```


Arg Arg Gly Pro Gly Lys Lys Glu Trp Gly Pro Gly Leu Pro Ser Gln
 50 55 60
 Ala Gln Asp Gly Ala Val Val Thr Ala Thr Arg Gln Ala Ser Arg Leu
 65 70 75 80
 Pro Glu Ala Glu Gly Leu Leu Pro Glu Gln Ser Pro Ala Gly Leu Leu
 85 90 95
 Gln Asp Lys Asp Leu Leu Leu Gly Leu Ala Leu Pro Tyr Pro Glu Lys
 100 105 110
 Glu Asn Arg Pro Pro Gly Trp Glu Arg Thr Arg Lys Arg Ser Arg Glu
 115 120 125
 His Lys Arg Arg Arg Asp Arg Leu Arg Leu His Gln Gly Arg Ala Leu
 130 135 140
 Val Arg Gly Pro Ser Ser Leu Met Lys Lys Ala Glu Leu Ser Glu Ala
 145 150 155 160
 Gln Val Leu Asp Ala Ala Met Glu Glu Ser Ser Thr Ser Leu Ala Pro
 165 170 175
 Thr Met Phe Phe Leu Thr Thr Phe Glu Ala Ala Pro Ala Thr Glu Glu
 180 185 190
 Ser Leu Ile Leu Pro Val Thr Ser Leu Arg Pro Gln Gln Ala Gln Pro
 195 200 205
 Arg Ser Asp Gly Glu Val Met Pro Thr Leu Asp Met Ala Leu Phe Asp
 210 215 220
 Trp Thr Asp Tyr Glu Asp Leu Lys Pro Asp Gly Trp Pro Ser Ala Lys
 225 230 235 240
 Lys Lys Glu Lys His Arg Gly Lys Leu Ser Ser Asp Gly Asn Glu Thr
 245 250 255
 Ser Pro Ala Glu Gly Glu Pro Cys Asp His His Gln Asp Cys Leu Pro
 260 265 270
 Gly Thr Cys Cys Asp Leu Arg Glu His Leu Cys Thr Pro His Asn Arg
 275 280 285
 Gly Leu Asn Asn Lys Cys Phe Asp Asp Cys Met Cys Val Glu
 290 295 300

<210> 311

<211> 670

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(670)

<400> 311

aat gtg act gta ttt gga aac agg gcc ttt aaa gaa gta att aag tat 576
 Asn Val Thr Val Phe Gly Asn Arg Ala Phe Lys Glu Val Ile Lys Tyr
 180 185 190

tac att cag tgt agg cat tca ata agt tca ggc tta gtg aag gtt gtc 624
 Tyr Ile Gln Cys Arg His Ser Ile Ser Ser Gly Leu Val Lys Val Val
 195 200 205

act gaa atc cca tca gct cag cag gga gca agg agc ctc ttt gaa a 670
 Thr Glu Ile Pro Ser Ala Gln Gln Gly Ala Arg Ser Leu Phe Glu
 210 215 220

<210> 312

<211> 223

<212> PRT

<213> Homo sapiens

<400> 312

Met Gly Met Val Tyr Ser Ser Ala Leu Leu Ser Leu Val Leu Val Ala
 1 5 10 15
 Met Val Leu Val Thr His Ser Gln Pro Trp Ser Glu Asn Arg Gly Gln
 20 25 30
 Ala Ala Ala Ser Leu Cys Ser Gln Pro Glu Lys Gln Pro Ser Lys Arg
 35 40 45
 Ile Gln Cys Gly Leu Ser Ser Glu Leu Asp Thr Leu Pro His Val Cys
 50 55 60
 Met Ser Val Pro Leu Leu Ile Gly Val Ser Gly Ile Gly Ala Ile Tyr
 65 70 75 80
 Gln Leu Asn Ser Ser Pro Met Thr Thr Val Met Thr Arg Ala Pro Gly
 85 90 95
 Ser Pro Val Leu Gln Ala Leu Asp Phe Ile Phe Tyr Val Asn Lys Met
 100 105 110
 Lys Met Asn Val Glu Glu Met Trp Lys Gly Met Ser Gly Thr Ser Phe
 115 120 125
 Phe Ala Leu Pro Arg Lys Lys Asp Ile Leu Pro Arg Trp Leu Arg Gly
 130 135 140
 Lys Gln Leu Val Lys Phe Gln Asn Thr Lys Ser Gln Ser Arg Glu Ser
 145 150 155 160
 Cys Ser Leu Pro Asn Leu His Val Glu Val Ile Asn Pro Val Ile Leu
 165 170 175
 Asn Val Thr Val Phe Gly Asn Arg Ala Phe Lys Glu Val Ile Lys Tyr

180 185 190
 Tyr Ile Gln Cys Arg His Ser Ile Ser Ser Gly Leu Val Lys Val Val
 195 200 205
 Thr Glu Ile Pro Ser Ala Gln Gln Gly Ala Arg Ser Leu Phe Glu
 210 215 220

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<210> 313
<211> 426
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (1)...(426)

<400> 313

atg gaa ggg gac ccc ggg ggg ttg ctg ctg ctg ctg ctg gct ggg gtg 48
Met Glu Gly Asp Pro Gly Gly Leu Leu Leu Leu Leu Leu Ala Gly Val
1 5 10 15

ggg gga tat cag ctg gga act aga agg aac ttc tcc cat gga gaa aag 96
Gly Gly Tyr Gln Leu Gly Thr Arg Arg Asn Phe Ser His Gly Glu Lys
20 25 30

gta aac gat aag atc cca gta gcc acc atc agc atc tgg gac aaa tac 144
Val Asn Asp Lys Ile Pro Val Ala Thr Ile Ser Ile Trp Asp Lys Tyr
35 40 45

agc cct cac cac tgg ggt ccc ctg cag tcc tca cag gca cta agc cca 192
Ser Pro His His Trp Gly Pro Leu Gln Ser Ser Gln Ala Leu Ser Pro
50 55 60

cct gag gga gct aac tgg agc cca cac agc tgt gct gtc tcc aca aaa 240
Pro Glu Gly Ala Asn Trp Ser Pro His Ser Cys Ala Val Ser Thr Lys
65 70 75 80

gga gct gat act gtg cac tgc cct cgg tgg tcc acg cag cta cta tac 288
Gly Ala Asp Thr Val His Cys Pro Arg Trp Ser Thr Gln Leu Leu Tyr
85 90 95

tgc acc atc cta gaa cta gga cta cca cta gag tgt gcc tta cta caa 336
Cys Thr Ile Leu Glu Leu Gly Leu Pro Leu Glu Cys Ala Leu Leu Gln
100 105 110

ggc gtc aga ctc cag gat ctt gga ctt ttg gaa tct tgg att tac acc 384
 Gly Val Arg Leu Gln Asp Leu Gly Leu Leu Glu Ser Trp Ile Tyr Thr
 115 120 125

agt ggt cta cct gag gct ctt ggg cct ccg gcc ata gag tga 426
 Ser Gly Leu Pro Glu Ala Leu Gly Pro Pro Ala Ile Glu *
 130 135 140

<210> 314

<211> 141

<212> PRT

<213> Homo sapiens

<400> 314

Met Glu Gly Asp Pro Gly Gly Leu Leu Leu Leu Leu Leu Ala Gly Val
 1 5 10 15
 Gly Gly Tyr Gln Leu Gly Thr Arg Arg Asn Phe Ser His Gly Glu Lys
 20 25 30
 Val Asn Asp Lys Ile Pro Val Ala Thr Ile Ser Ile Trp Asp Lys Tyr
 35 40 45
 Ser Pro His His Trp Gly Pro Leu Gln Ser Ser Gln Ala Leu Ser Pro
 50 55 60
 Pro Glu Gly Ala Asn Trp Ser Pro His Ser Cys Ala Val Ser Thr Lys
 65 70 75 80
 Gly Ala Asp Thr Val His Cys Pro Arg Trp Ser Thr Gln Leu Leu Tyr
 85 90 95
 Cys Thr Ile Leu Glu Leu Gly Leu Pro Leu Glu Cys Ala Leu Leu Gln
 100 105 110
 Gly Val Arg Leu Gln Asp Leu Gly Leu Leu Glu Ser Trp Ile Tyr Thr
 115 120 125
 Ser Gly Leu Pro Glu Ala Leu Gly Pro Pro Ala Ile Glu
 130 135 140

<210> 315

<211> 375

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(375)

<400> 315
 atg gtc ctg tgc tgg ctg ctg ctt ctg gtg atg gct ctg ccc cca ggc 48
 Met Val Leu Cys Trp Leu Leu Leu Leu Val Met Ala Leu Pro Pro Gly
 1 5 10 15

 acg acg ggc gtc aag gac tgc gtc ttc tgt gag ctc acc gac tcc atg 96
 Thr Thr Gly Val Lys Asp Cys Val Phe Cys Glu Leu Thr Asp Ser Met
 20 25 30

 cag tgt cct ggt acc tac atg cac tgt ggc gat gac gag gac tgc ttc 144
 Gln Cys Pro Gly Thr Tyr Met His Cys Gly Asp Asp Glu Asp Cys Phe
 35 40 45

 aca ggc cac ggg gtc gcc ccg ggc act ggt ccg gtc atc aac aaa ggc 192
 Thr Gly His Gly Val Ala Pro Gly Thr Gly Pro Val Ile Asn Lys Gly
 50 55 60

 tgc ctg cga gcc acc agc tgc ggc ctt gag gaa ccc gtc agc tac agg 240
 Cys Leu Arg Ala Thr Ser Cys Gly Leu Glu Glu Pro Val Ser Tyr Arg
 65 70 75 80

 ggc gtc acc tac agc ctc acc acc aac tgc tgc acc ggc cgc ctg tgt 288
 Gly Val Thr Tyr Ser Leu Thr Thr Asn Cys Cys Thr Gly Arg Leu Cys
 85 90 95

 aac aga gcc ccg agc agc cag aca gtg ggg gcc acc acc agc ctg gca 336
 Asn Arg Ala Pro Ser Ser Gln Thr Val Gly Ala Thr Thr Ser Leu Ala
 100 105 110

 ctg ggg ctg ggt atg ctg ctt cct cca cgt ttg ctg tga 375
 Leu Gly Leu Gly Met Leu Leu Pro Pro Arg Leu Leu *
 115 120

<210> 316

<211> 124

<212> PRT

<213> Homo sapiens

<400> 316

Met Val Leu Cys Trp Leu Leu Leu Leu Val Met Ala Leu Pro Pro Gly
 1 5 10 15

Thr Thr Gly Val Lys Asp Cys Val Phe Cys Glu Leu Thr Asp Ser Met
 20 25 30
 Gln Cys Pro Gly Thr Tyr Met His Cys Gly Asp Asp Glu Asp Cys Phe
 35 40 45
 Thr Gly His Gly Val Ala Pro Gly Thr Gly Pro Val Ile Asn Lys Gly
 50 55 60
 Cys Leu Arg Ala Thr Ser Cys Gly Leu Glu Glu Pro Val Ser Tyr Arg
 65 70 75 80
 Gly Val Thr Tyr Ser Leu Thr Thr Asn Cys Cys Thr Gly Arg Leu Cys
 85 90 95
 Asn Arg Ala Pro Ser Ser Gln Thr Val Gly Ala Thr Thr Ser Leu Ala
 100 105 110
 Leu Gly Leu Gly Met Leu Leu Pro Pro Arg Leu Leu
 115 120

<210> 317

<211> 688

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(688)

<400> 317

atg gag ccc ctg cgc gcg ccc gcg ctg cgc cgc ctg ctg ccg ccg ctg 48
 Met Glu Pro Leu Arg Ala Pro Ala Leu Arg Arg Leu Leu Pro Pro Leu
 1 5 10 15

ctg ctc ctg ctg ctg tca ctg ccc ccc cgc gcc cgg gcc aag tac gtg 96
 Leu Leu Leu Leu Leu Ser Leu Pro Pro Arg Ala Arg Ala Lys Tyr Val
 20 25 30

cgg ggc aac ctc agt tcc aag gag gac tgg gtg ttc ctg aca aga ttt 144
 Arg Gly Asn Leu Ser Ser Lys Glu Asp Trp Val Phe Leu Thr Arg Phe
 35 40 45

tgt ttc ctc tcg gat tac ggc cga ctg gac ttc cgt ttc cgc tac cct 192
 Cys Phe Leu Ser Asp Tyr Gly Arg Leu Asp Phe Arg Phe Arg Tyr Pro
 50 55 60

gag gcc aag tgc tgt cag aac atc ctc ctc tat ttt gat gac cca tcc 240
 Glu Ala Lys Cys Cys Gln Asn Ile Leu Leu Tyr Phe Asp Asp Pro Ser

<221> CDS

<222> (1)...(765)

<400> 319

atg gga gct cca aag ctg gcc aag ctg cac aca gcc ctg ctg gcg tcc	48
Met Gly Ala Pro Lys Leu Ala Lys Leu His Thr Ala Leu Leu Ala Ser	
1 5 10 15	

agc ctg gct cta ggc cag gag cct tgg ctg gag ggc ggc cca gcg ccc	96
Ser Leu Ala Leu Gly Gln Glu Pro Trp Leu Glu Gly Gly Pro Ala Pro	
20 25 30	

cga cag cca cgt cca gca cct tca gca ggt tct ccc cgg cag cac ttg	144
Arg Gln Pro Arg Pro Ala Pro Ser Ala Gly Ser Pro Arg Gln His Leu	
35 40 45	

gca gtc aga tgt ggc cag acg gtc cct tcc aga gag agc tgt cgt ggc	192
Ala Val Arg Cys Gly Gln Thr Val Pro Ser Arg Glu Ser Cys Arg Gly	
50 55 60	

ccc aaa ggc atg aac gtg gcc ctc cgt gca cgg caa gca gta cag gaa	240
Pro Lys Gly Met Asn Val Ala Leu Arg Ala Arg Gln Ala Val Gln Glu	
65 70 75 80	

cgt gtt cgg aag gca gag tgc gcg gcc aac agc tgt gct gcc ctg gac	288
Arg Val Arg Lys Ala Glu Cys Ala Ala Asn Ser Cys Ala Ala Leu Asp	
85 90 95	

aag tgc cct cca cct caa cag ttt ccc ctg caa ggc ctc cat gat gag	336
Lys Cys Pro Pro Pro Gln Gln Phe Pro Leu Gln Gly Leu His Asp Glu	
100 105 110	

cgg aac aca gcc act cct ggg gaa ggg cac aag cag cag tca cac gtc	384
Arg Asn Thr Ala Thr Pro Gly Glu Gly His Lys Gln Gln Ser His Val	
115 120 125	

gca ctg aag tgg ctg gat gga cgc cag aga gtc cag agg cag aca gga	432
Ala Leu Lys Trp Leu Asp Gly Arg Gln Arg Val Gln Arg Gln Thr Gly	
130 135 140	

aac aca aaa tgg aag atg ctg gtg cac gca gaa agt ctt gga gga gga	480
Asn Thr Lys Trp Lys Met Leu Val His Ala Glu Ser Leu Gly Gly Gly	
145 150 155 160	

gag cca gaa acc ttc aca aaa tcc aaa tca gac ctc gtc tct gct cac 528
 Glu Pro Glu Thr Phe Thr Lys Ser Lys Ser Asp Leu Val Ser Ala His
 165 170 175

ttc acc ccg tcg cag ctt ctt acg ctc ccc ccc att ttt aca gac aag 576
 Phe Thr Pro Ser Gln Leu Leu Thr Leu Pro Pro Ile Phe Thr Asp Lys
 180 185 190

gaa act gag tcc cag agg ccc gga aat ggg gag ggc ggg gag tca gga 624
 Glu Thr Glu Ser Gln Arg Pro Gly Asn Gly Glu Gly Gly Glu Ser Gly
 195 200 205

cag gtg gca gga aca ggg ctg cct cta ggg caa ctg atg aac cct ggc 672
 Gln Val Ala Gly Thr Gly Leu Pro Leu Gly Gln Leu Met Asn Pro Gly
 210 215 220

agc agc atc cgt gac act gga gag ccc aac acc agc tgc cac tgt gtg 720
 Ser Ser Ile Arg Asp Thr Gly Glu Pro Asn Thr Ser Cys His Cys Val
 225 230 235 240

gcc ctg tgg cat tgg cca caa atg agc aca tcc atc agc tcc tga 765
 Ala Leu Trp His Trp Pro Gln Met Ser Thr Ser Ile Ser Ser *
 245 250

<210> 320

<211> 254

<212> PRT

<213> Homo sapiens

<400> 320

Met Gly Ala Pro Lys Leu Ala Lys Leu His Thr Ala Leu Leu Ala Ser
 1 5 10 15
 Ser Leu Ala Leu Gly Gln Glu Pro Trp Leu Glu Gly Gly Pro Ala Pro
 20 25 30
 Arg Gln Pro Arg Pro Ala Pro Ser Ala Gly Ser Pro Arg Gln His Leu
 35 40 45
 Ala Val Arg Cys Gly Gln Thr Val Pro Ser Arg Glu Ser Cys Arg Gly
 50 55 60
 Pro Lys Gly Met Asn Val Ala Leu Arg Ala Arg Gln Ala Val Gln Glu
 65 70 75 80
 Arg Val Arg Lys Ala Glu Cys Ala Ala Asn Ser Cys Ala Ala Leu Asp

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<210> 321
<211> 339
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (1)...(339)

<400> 321																
atg	gtg	ctc	acc	aat	acg	gct	tct	ttc	tat	gca	gct	ctg	cag	cta	ctg	48
Met	Val	Leu	Thr	Asn	Thr	Ala	Ser	Phe	Tyr	Ala	Ala	Leu	Gln	Leu	Leu	
1			5			10			15							
ctg	gct	ctt	ctg	gga	att	ttt	tct	ttt	gta	tat	ccg	tcc	ctg	gtg	gat	96
Leu	Ala	Leu	Leu	Gly	Ile	Phe	Ser	Phe	Val	Tyr	Pro	Ser	Leu	Val	Asp	
			20			25						30				
cac	ttg	ccc	ttt	cct	gcc	aaa	ccc	ttg	cct	ctg	tct	gaa	ttc	tgg	ttt	144
His	Leu	Pro	Phe	Pro	Ala	Lys	Pro	Leu	Pro	Leu	Ser	Glu	Phe	Trp	Phe	
35						40						45				

Met	Val	Leu	Thr	Asn	Thr	Ala	Ser	Phe	Tyr	Ala	Ala	Leu	Gln	Leu	Leu
1				5					10					15	
Leu	Ala	Leu	Leu	Gly	Ile	Phe	Ser	Phe	Val	Tyr	Pro	Ser	Leu	Val	Asp
			20					25					30		
His	Leu	Pro	Phe	Pro	Ala	Lys	Pro	Leu	Pro	Leu	Ser	Glu	Phe	Trp	Phe
		35					40					45			
Gly	Ser	Ser	Phe	Val	Ala	Pro	Arg	Ala	Ser	Ala	Asn	Leu	Val	Gly	Ala
	50					55					60				
Phe	Ala	Ala	Ile	Gly	Lys	Arg	Ser	Pro	Phe	Phe	Arg	Ala	Pro	Met	Ile
65					70					75					80
Leu	Lys	Gln	Arg	Leu	Met	Lys	Thr	His	Glu	Trp	Val	Ser	Thr	Pro	Ile
				85					90					95	
His	Pro	Leu	Cys	Gln	Ala	Leu	Val	Glu	Thr	Thr	Val	His	Asp	Pro	Glu
			100					105					110		

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<220>
<221> CDS
<222> (1)...(888)
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atg cgc ctc cac ctg ctc ctg ctg ctc gcg ctg tgc ggt gca ggc acc 48
Met Arg Leu His Leu Leu Leu Leu Leu Ala Leu Cys Gly Ala Gly Thr
1 5 10 15

acc gcc gcg gag ctc agt tac agc ttg cgt ggc aac tgg agc atc tgc 96
Thr Ala Ala Glu Leu Ser Tyr Ser Leu Arg Gly Asn Trp Ser Ile Cys
20 25 30

aat ggg aac ggc tcg ctg gag ctg ccc ggg gcg gtc cct ggc tgc gtg 144
Asn Gly Asn Gly Ser Leu Glu Leu Pro Gly Ala Val Pro Gly Cys Val
35 40 45

cac agc gcc ttg ttc cag cag ggc ctg atc cag gtc act ctg ttg tgt 192
His Ser Ala Leu Phe Gln Gln Gly Leu Ile Gln Val Thr Leu Leu Cys
50 55 60

gaa ggc tac agt gca gga gag tgg aag cct gga gac caa cca ggg gac 240
Glu Gly Tyr Ser Ala Gly Glu Trp Lys Pro Gly Asp Gln Pro Gly Asp
65 70 75 80

tat tgc tgg tct atg tat ggg caa gag atg act tct ggc ttg gac aag 288
Tyr Cys Trp Ser Met Tyr Gly Gln Glu Met Thr Ser Gly Leu Asp Lys
85 90 95

cat ggt ggc agt gaa atg ctc caa aca cat ttc tac acc gat aac aag 336
His Gly Gly Ser Glu Met Leu Gln Thr His Phe Tyr Thr Asp Asn Lys
100 105 110

aaa tat gct gta aat gat gtt tcc ttc tca atc cct gcc gcc tct gaa 384
Lys Tyr Ala Val Asn Asp Val Ser Phe Ser Ile Pro Ala Ala Ser Glu
115 120 125

ttt gct gac ctt agt aac atc atc aat aaa tta cta aag gac aaa aat 432

<400> 324															
Met 1	Arg	Leu	His	Leu 5	Leu	Leu	Leu	Leu	Ala 10	Leu	Cys	Gly	Ala	Gly 15	Thr
Thr	Ala	Ala	Glu 20	Leu	Ser	Tyr	Ser	Leu 25	Arg	Gly	Asn	Trp	Ser 30	Ile	Cys
Asn	Gly	Asn	Gly 35	Ser	Leu	Glu	Leu 40	Pro	Gly	Ala	Val	Pro 45	Gly	Cys	Val
His	Ser	Ala	Leu	Phe	Gln	Gln	Gly 55	Leu	Ile	Gln	Val 60	Thr	Leu	Leu	Cys
Glu 65	Gly	Tyr	Ser	Ala	Gly	Glu	Trp 70	Lys	Pro	Gly	Asp	Gln	Pro	Gly	Asp 80
Tyr	Cys	Trp	Ser	Met 85	Tyr	Gly	Gln	Glu 90	Met	Thr	Ser	Gly	Leu 95	Asp	Lys
His	Gly	Gly	Ser 100	Glu	Met	Leu	Gln	Thr 105	His	Phe	Tyr	Thr	Asp 110	Asn	Lys
Lys	Tyr	Ala	Val 115	Asn	Asp	Val	Ser	Phe 120	Ser	Ile	Pro	Ala	Ala 125	Ser	Glu
Phe	Ala	Asp	Leu	Ser	Asn	Ile	Ile 135	Asn	Lys	Leu	Leu 140	Lys	Asp	Lys	Asn
Glu 145	Phe	His	Lys	His	Met	Glu	Phe	Tyr	Phe	Leu	Ile	Lys	Gly	Gln	Phe 160
Leu	Arg	Met	Ser	Leu 165	Val	Lys	His	Met	Glu	Leu	Glu	Asn	Met	Ser	Ser
Glu	Val	Val	Val 180	Glu	Ile	Glu	Tyr	Val 185	Lys	Tyr	Thr	Ala	Pro 190	Gln	Pro
Glu	Gln	Cys	Met 195	Phe	His	Asp	Asp	Trp 200	Ile	Leu	Ser	Val	Lys 205	Gly	Ala
Lys	Glu	Trp	Ile 210	Leu	Thr	Gly	Ser	Tyr 215	Asp	Lys	Thr	Ser	Gln 220	Ile	Arg
Ser 225	Leu	Glu	Arg	Lys	Ser	Ile	Met	Thr	Ile	Val	Gly	His	Arg	Asp	Val 240
Leu	Lys	Asp	Val 245	Ala	Trp	Ala	Lys	Lys	Lys	Asp	Ser	Leu	Ser	Cys	Leu
Phe	Val	Ser	Ala 260	Ser	Met	Asp	Pro	Thr 265	Ile	Leu	Leu	Trp	Glu	Trp	Asn
Arg	Glu	Lys	Gln 275	Ser	Glu	Ser	Pro	Thr	Val	Leu	Gln	Arg	Ser	Cys	Trp

Lys Cys Arg Val Tyr Ser Cys
290 295

<210> 325
<211> 549
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(549)

<400> 325

atg gag gct gaa aga cta agc cag tct agt ctg tcc atg ttc ctc tgc 48
Met Glu Ala Glu Arg Leu Ser Gln Ser Ser Leu Ser Met Phe Leu Cys
1 5 10 15

ctg ctt ttt att cta tcc gtg ctg gca gct gat gag atg atg ccc acc 96
Leu Leu Phe Ile Leu Ser Val Leu Ala Ala Asp Glu Met Met Pro Thr
20 25 30

cag att gag gct act att acc ttc ttg ctt gtc acg ttg ctc att tac 144
Gln Ile Glu Ala Thr Ile Thr Phe Leu Leu Val Thr Leu Leu Ile Tyr
35 40 45

tcc tca ggg cca gct agg tgc ctg gag tct ccc ctg aaa gaa ctc aag 192
Ser Ser Gly Pro Ala Arg Cys Leu Glu Ser Pro Leu Lys Glu Leu Lys
50 55 60

att ttc ctt tat ttt cat gct cag cgc ggg ggt gcg gca gag gtc cct 240
Ile Phe Leu Tyr Phe His Ala Gln Arg Gly Gly Ala Ala Glu Val Pro
65 70 75 80

gct ctg tct cac tgg gac tat caa gtg tct ggt aca gaa aat aga gca 288
Ala Leu Ser His Trp Asp Tyr Gln Val Ser Gly Thr Glu Asn Arg Ala
85 90 95

act caa tgc agt tgc cgg ttt cag agc att ctt gaa ttg atc gtg aaa 336
Thr Gln Cys Ser Cys Arg Phe Gln Ser Ile Leu Glu Leu Ile Val Lys
100 105 110

cag ctt tcc agg tgc gat cgt ata aag gat cat tgg cag ctg tgc agc 384
Gln Leu Ser Arg Cys Asp Arg Ile Lys Asp His Trp Gln Leu Cys Ser

115 120 125
 ttg tca gct agc tgc aga aac cca ggt gtc atg ctg aca gct tca gtg 432
 Leu Ser Ala Ser Cys Arg Asn Pro Gly Val Met Leu Thr Ala Ser Val
 130 135 140

tta ata gcc ttt cag act tgg aga gcc agc atc cga cat aaa aat gat 480
 Leu Ile Ala Phe Gln Thr Trp Arg Ala Ser Ile Arg His Lys Asn Asp
 145 150 155 160

agt ctt ata gag ttt gtt aat cag ctc tca aca ctg tgt aag aat aga 528
 Ser Leu Ile Glu Phe Val Asn Gln Leu Ser Thr Leu Cys Lys Asn Arg
 165 170 175

ccc ctg gat cgg ctt ctg tga 549
 Pro Leu Asp Arg Leu Leu *
 180

<210> 326

<211> 182

<212> PRT

<213> Homo sapiens

<400> 326

Met Glu Ala Glu Arg Leu Ser Gln Ser Ser Leu Ser Met Phe Leu Cys
 1 5 10 15
 Leu Leu Phe Ile Leu Ser Val Leu Ala Ala Asp Glu Met Met Pro Thr
 20 25 30
 Gln Ile Glu Ala Thr Ile Thr Phe Leu Leu Val Thr Leu Leu Ile Tyr
 35 40 45
 Ser Ser Gly Pro Ala Arg Cys Leu Glu Ser Pro Leu Lys Glu Leu Lys
 50 55 60
 Ile Phe Leu Tyr Phe His Ala Gln Arg Gly Gly Ala Ala Glu Val Pro
 65 70 75 80
 Ala Leu Ser His Trp Asp Tyr Gln Val Ser Gly Thr Glu Asn Arg Ala
 85 90 95
 Thr Gln Cys Ser Cys Arg Phe Gln Ser Ile Leu Glu Leu Ile Val Lys
 100 105 110
 Gln Leu Ser Arg Cys Asp Arg Ile Lys Asp His Trp Gln Leu Cys Ser
 115 120 125
 Leu Ser Ala Ser Cys Arg Asn Pro Gly Val Met Leu Thr Ala Ser Val
 130 135 140

Leu Ile Ala Phe Gln Thr Trp Arg Ala Ser Ile Arg His Lys Asn Asp
 145 150 155 160
 Ser Leu Ile Glu Phe Val Asn Gln Leu Ser Thr Leu Cys Lys Asn Arg
 165 170 175
 Pro Leu Asp Arg Leu Leu
 180

<210> 327
 <211> 681
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(681)

<400> 327

atg gtg agt tct tgg gga ggg gga gtc tct tac aga cac ctg ggg ctc 48
 Met Val Ser Ser Trp Gly Gly Gly Val Ser Tyr Arg His Leu Gly Leu
 1 5 10 15

ttg atc ctg gca ctg ctg gcc ctc ctc acc cta ctg ggt gtt gtt ctg 96
 Leu Ile Leu Ala Leu Leu Ala Leu Leu Thr Leu Leu Gly Val Val Leu
 20 25 30

gcc ctc acc tgc cgg cgc cca cag tca ggc ccg ggc cca gcg cgg cca 144
 Ala Leu Thr Cys Arg Arg Pro Gln Ser Gly Pro Gly Pro Ala Arg Pro
 35 40 45

gtg ctc ctc ctg cac gcg gcg gac tcg gag gcg cag cgg cgc ctg gtg 192
 Val Leu Leu Leu His Ala Ala Asp Ser Glu Ala Gln Arg Arg Leu Val
 50 55 60

gga gcg ctg gct gaa ctg cta cgg gca gcg ctg ggc ggc ggg cgc gac 240
 Gly Ala Leu Ala Glu Leu Leu Arg Ala Ala Leu Gly Gly Gly Arg Asp
 65 70 75 80

gtg atc gtg gac ctg tgg gag ggg agg cac gtg gcg cgc gtg ggc ccg 288
 Val Ile Val Asp Leu Trp Glu Gly Arg His Val Ala Arg Val Gly Pro
 85 90 95

ctg ccg tgg ctc tgg gcg gcg cgg acg cgc gta gcg cgg gag cag ggc 336
 Leu Pro Trp Leu Trp Ala Ala Arg Thr Arg Val Ala Arg Glu Gln Gly

100 105 110
 act gtg ctg ctg ctg tgg agc ggc gcc gac ctt cgc ccg gtc agc ggc 384
 Thr Val Leu Leu Leu Trp Ser Gly Ala Asp Leu Arg Pro Val Ser Gly
 115 120 125
 ccc gac ccc cgc gcc gcg ccc ctg ctc gcc ctg ctc cac gct gcc ccg 432
 Pro Asp Pro Arg Ala Ala Pro Leu Leu Ala Leu Leu His Ala Ala Pro
 130 135 140
 cgc ccg ctg ctg ctg ctc gct tac ttc agt cgc ctc tgc gcc aag ggc 480
 Arg Pro Leu Leu Leu Leu Ala Tyr Phe Ser Arg Leu Cys Ala Lys Gly
 145 150 155 160
 gac atc ccc ccg ccg ctg cgc gcc ctg ccg cgc tac cgc ctg ctg cgc 528
 Asp Ile Pro Pro Pro Leu Arg Ala Leu Pro Arg Tyr Arg Leu Leu Arg
 165 170 175
 gac ctg ccg cgt ctg ctg cgg gcg ctg gac gcg cgg cct ttc gca gag 576
 Asp Leu Pro Arg Leu Leu Arg Ala Leu Asp Ala Arg Pro Phe Ala Glu
 180 185 190
 gcc acc agc tgg ggc cgc ctt ggg gcg cgg cag cgc agg cag agc cgc 624
 Ala Thr Ser Trp Gly Arg Leu Gly Ala Arg Gln Arg Arg Gln Ser Arg
 195 200 205
 cta gag ctg tgc agc cgg ctt gaa cga gag gcc gcc cga ctt gca gac 672
 Leu Glu Leu Cys Ser Arg Leu Glu Arg Glu Ala Ala Arg Leu Ala Asp
 210 215 220
 cta ggt tga 681
 Leu Gly *
 225

<210> 328
 <211> 226
 <212> PRT
 <213> Homo sapiens

<400> 328
 Met Val Ser Ser Trp Gly Gly Gly Val Ser Tyr Arg His Leu Gly Leu
 1 5 10 15

Glu Tyr Met Pro Met Glu
1 5